

APR 19 2007

ENTER 1600/290

- 4862 AGGGAACAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCGAGG
TCCCTGCTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCGGACGATGAGGTATCTT
4893 BGL2,
- ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAGTGAAGTGTG
4954 NCOI,
- SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACCTGGGGTAGCC
TCAATGAGAGGTCCACTTTAGTTATCCACCGGCGTACGGAGTCTTTGAACCCCATGGC
5015 SPHI, 5035 KPNI,
- ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGGCAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
GGGAACGCTCGAACCTCTGTGGCCCGGGCTCGCAGGCGCGATCCGAAGACCGGTCTCTCT
5064 APAI, 5091 BALI,
- GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAGCTCAAA
CCGTCCCGACGGTATACACCGTTCTATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
5113 NDEI,
- LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162 CTCACTCCAATAGCGGCGCTGGCCAGCTGGACTTGTCCGGCTGGTTACCGGCTGGCTAC
GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCGCAAGTGCCGACCGATG
5174 NOTI, 5175 EAGI XMA3, 5182 BALI, 5186 PVU2,
- SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCGCTGGATCTGGTTTTGC
TCGCCCCCTCTGTAATAGTGTGCGCACAGAGTACGGGCGGGGCGACCTAGACCAAAACG
5240 DRA3,
- LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCCTCCCAACCGAATGAGCAGCAAT
GATGAGGACGAACGACGCTCCCATCCGTAGATGGAGGAGGGTTGGCTTACTCGTGCTTA
5295 PSTI,
- ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342 CCTAAACCTCAAAGAAAGACCAACGTAACACCAACCGGCGGCGCAGGACGTCAGTTTC
GGATTTGGAGTTTCTTCTGTTTGCAATTGTGGTTGGCCGCGCGCTCGCAGTTCAGG
5380 NOTI, 5381 EAGI XMA3, 5390 AAT2, 5401 SMAI XMAI,
- ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402 CCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
GGCCCAACCGGCTAGCAACCAACCTCAAATGAACAACGGCGCGTCCCGGGATCTAAC

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TECH CENTER 1600/2900

4229 DRD1, 4236 ALWN1,
 GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
 4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCAAGCCCGCGTGGCCATCAAGTCC
 CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTGCGGCGCACCGGTAGTTCAGG
 4301 BGLI, 4308 BALI,
 LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
 4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAGCTCGCGC
 GAGTGGCTCTCCGAAATACAACCCCGGAGAATGGTTAAGTTCGCCCTCTTGACGCCG
 4345 APAI,
 TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 4382 TATCGCAGGTGCCGCGCAGCGGCTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
 TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 4442 TACATCAAGGCCCGGCGAGCCTGTCGAGCCGAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCGGGGCCCTCGGACAGCTCGGCGTCCCGAGGTCTGACGTGGTACGAGCAC
 4452 SMAI XMAI,
 CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCAGCACTTAGTCGTTACTGTGAAAGCGCGGGGTCAGGAGGACGCGCGCAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCAGGTCTCTGCGCCGCTCG
 4508 DRD1, 4511 TTH3I,
 LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCTCCGATACTGGTCCATGAGCGGGGGGACCCCTGGGGGTGTT
 ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTGCACAGTCAGCGGGTGCTG
 4637 SACI,
 GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
 4682 GCGCTGGAAAGAGGGTCTACTACCTACCCGTGACCTACAACCCCTCGCGAGAGCT
 CCGCACCTTTCTCCAGATGATGGAGTGGGCACTGGGATGTGGGGGGAGCGCTCTCGA
 4731 NRUI,
 AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 4742 GCGTGGGAGACAGACACACTCCAGTCAATTCTGGCTAGGCAACATAATCATGTTT
 CGCACCTCTGTGCTTCTGTGTGAGGTGAGTTAAGGACCGATCCGTTGTATTAGTACAAA
 AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
 4802 GCCCCACACTGTGGGCGAGGATGATACTGATGACCATTTCTTTAGCGTCTTTATAGCC
 CGGGGGTGTGACACCCCTCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
 4806 PFLM1, 4807 DRA3,
 ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

3589 DRA3, 3600 SAC2,

AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
 3602 GCGGAAGAACAGAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCAAT
 CGCCTTCTTGCTTTGACGGGTAGTTACGTGATTTCGTTGAGCAACGATGCAGTGGTGA
 3611 ALWN1, 3655 PFLM1,

LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
 3662 TTGGTGTTATCCACCACTCACGCAGTGCTTGCCAAAGGCAGAGAAAGTCACATTGAC
 AACCACATAAGGTGGTGGAGTGCCTCAGCAACGGTTTCCGTCTCTTTTCAGTGTAAGTGC
 3681 DRA3,

ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
 3722 AGACTGCAAGTTCTGGACAGCCATTACCAAGGACGTACTCAAGAGGTTAAAGCAGCGGGC
 TCTGACGTTCAAGACCTGTCGGTAATGGTCTCGATGAGTTCTCTCAATTTCGTCGCGGC

SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
 3782 TCAAAAGTGAAGGCTAAGTTGCTATCCGTAGAGGAAGCTTGACAGCTGACGCCCCCAGC
 AGTTTTCTACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
 3816 HIND3,

SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
 3842 TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCGCTGGCCATGCCAGAAAGGCC
 AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
 3875 AAT2, 3890 BGLI,

ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
 3902 GTAACCCACATCAACTCCGTGTGGAAGACCTTCTGGAAGACAAATGTAACACCAATAGAC
 CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG

ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
 3962 ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTACGCTGAGAGAGGGGGTCTGAAG
 TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCAGCATTC

ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
 4022 CCAGCTCGTCTCATCGTGTCCCCGATCTGGGCGTGCCTGTCGGAAGATGGCTTTG
 GGTGAGCAGAGTAGCACAGGGGGCTAGACCCGACGCGCACACGCTTTTCTACCGAAAC

TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
 4082 TACGAGCTGGTTACAAAGCTCCCTTGCGCGTGATGGGAAGCTCCTACGGATTCCAATAC
 ATGTGACCAATGTTTCGAGGGGAACCGGCACTACCTTCGAGGATGCTTAAGGTTATG

SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
 4142 TCACCAGGACAGCGGGTTGAATTCTCGTCAAGCGTGGGAAGTCCAAGAAAACCCCAATG
 AGTGGTCTGTGCCCCAACTTAAGGAGCACGTTTCGACCTTCAGGTTCTTTTGGGGGTAC
 4160 ECORI,

GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
 4202 GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
 CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCTGAGTACTCTCGCTGTAGGCATGC

FIG. 22—Page 7

ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
 2942 ACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
 TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
 2966 ESPI, 2969 SACI,
 GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
 3002 GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAGTGGTGATTCTGGACTCC
 CTCTACCCGCGCTTGTAGTGGTCCCAACTCAGTCTTTTGTTCACCCTAAGACCTGAGG
 PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 3062 TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGAGAAATCCTG
 AAGCTAGGCGAACACCGCCTCCTCTGCTGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
 3096 BGL2,
 ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
 3122 CGGAAGTCTCGGAGATTGCGCCAGGCCCTGCCCGTTTGGGCGCGCGGACTATAACCC
 GCCTTCAGAGCCTCTAAGCGGGTCCGGACGGGCAACCGCGCGGCTGATATTGGGG
 3143 ALWN1, 3164 EAG1 XMA3,
 ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
 3182 CCGCTAGTGGAGACGTGGAAGAGCCCGACTACGAACCACTGTGGTCCATGGCTGCCCG
 GCGCATACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAAGTACCGAGCGGC
 3217 HGIE2, 3229 NCOI,
 LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
 3242 CTTCCACCTCCAAGTCCCTCCTGTGCTCCGCTCGGAAGAGCGGACGGTGGTCTC
 GAAGGTGGAGGTTTCAGGGGAGGACACGGAGCGGAGCCTTCTTCGCTGCCACCAAGGAG
 ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
 3302 ACTGAATCAACCCTATCTACTGCGCTTGGCCGAGCTCGCCACCAAGCTTTGGCAGCTCC
 TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAACCGTCGAGG
 3332 SACI, 3346 HIND3,
 SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
 3362 TCAACTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGGCCGCCCTTCTGGC
 AGTTGAAGGCCGTAAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGGGGGAAGACCG
 CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
 3422 TGCCCCCGGACTCCGACGCTGAGTCTTCTCCTCATGCCCGGCTGGAGGGGGAGCCT
 ACGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
 3437 EAM11051,
 GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
 3482 GGGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCCAACCGGGAG
 CCCATAGGCTAGAAATCGCTGCCAGTACCAAGTGCAGTCTACTCCGGTTGCGCCTC
 3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
 AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
 3542 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTACCCCGTGGCGCC
 CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCAGCGCG

3589 DRA3, 3600 SAC2,

3602 AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
CGCGAAGAAGCAGAACTGCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCAACAAT
CGCCTTCTGTCTTTACGGGTAGTTACGTGATTCTGTTAGCAACGATGCAAGTGGTGTTA

3611 ALWN1, 3655 PFLM1,

3662 LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
TTGGTGATTCCACCACCTCACGCAAGTCTTGCCTAAGGCAGAGAAAGTCACATTTGAC
AACCACATAAAGGTGGTGGAGTGCCTCAGAACGGTTTCCGTCTCTTTCACTGTAAGTGC

3681 DRA3,

3722 ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGAGGTTAAAGCAGCGGCG
TCTGACGTTCAAGACCTGTCGGTAATGGTCTCGCATGAGTTCCTCCAATTCGTCGCGCG

3782 SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
TCAAAGTGAAGGCTAAGTTGCTATCCGTAGAGGAAGCTTGACGCTGACGCCCCACAC
AGTTTTCTACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTCGGGGGTGTG

3816 HIND3,

3842 SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAGACGTCGCTTGCCATGCCAGAAAGGCC
AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG

3875 AAT2, 3890 BGLI,

3902 ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
GTAACCCACATCAACTCCGTGTGGAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG

3962 ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
ACTACCATCATGGCTAAGAAGCAGGTTTTCTGCGTTGAGCCTGAGAAAGGGGGTTCGTAAG
TGATGGTAGTACCGATTCTTGCTCCAAAGACGCAAGTCGGACTCTTCCCCCAGCATTCT

4022 ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
CCAGCTCGTCTCATCGTGTCCCGCATCTGGGCGTGCAGCGTGTGCGAAAGATGGCTTTG
GGTCGAGCAGAGTAGCACAGGGGCTAGACCCGACGCGCACAGCTTTTCTACCGAAAC

4082 TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
TACGACGTGGTTACAAAGCTCCCTTGGCCGTGATGGGAAGCTCCTACGGATCCCAATAC
ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCTTCGAGGATGCCTAAGGTTATG

4142 SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAAGTCCAAGAAAACCCCAATG
AGTGGTCTGTGCCCAACTTAAGGAGCAGGTTTCGACCTTCAGGTTCTTTTGGGGTTAC

4160 ECORI,

4202 GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
CCCAAGAGCATACTATGGGCGACGAACTGAGGTGTGCTGACTCTCGCTGTAGGCATGC

2342 LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
 AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGTGCCACTGTGGAGCTGAGATC
 TTCCCCAGACCGCTCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
 ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
 2402 ACTGGACATGTCAAACGGGACGATGAGGATCGTCCGTCCTAGGACCTGCAGGAACATG
 TGACCTGTACAGTTTTTGCCCTGCTACTCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
 TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
 2462 TGGAGTGGGACCTTCCCCATTAATGCTACACCACGGGCCCTGTACCCCCCTTCCTGCG
 ACCTCACCTTGAAGGGGTAATTACGGATGTGGTGCCCGGGACATGGGGGGAAGGACGC
 2480 ASE1, 2497 APAI,
 ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 2522 CCGAATACACGTTCCGCGTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTGTATGTGAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
 2553 PSTI,
 ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
 CACCCCCGTAAGGTGATGCACCTGCCATCTATGACTGTTAGAAATTTACGGGCACGGTC
 2594 DRA3,
 ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
 2642 GTCCCATCGCCCCGAATTTTACAGAAATGGACGGGGTGCGCCATACATAGGTTTGCGCC
 CAGGGTAGCGGGCTTAAAGGTGCTTAACTGCCACGCGGATGTATCCAAACGCGGG
 ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTACAGTAGGACTCCACGAATACCCG
 GGGACGTTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTTATGGGC
 2757 HGIE2,
 ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
 2762 GTAGGGTCGAATTAACCTTGCAGCCCCGAACCGGACGTGGCCGTGTTAGCTCCATGCTC
 CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACCTCAGGTACGAG
 2809 AAT2,
 ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGCGCGGCGAAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGTATATTGTCGTCTCCGCGGCCGCTTCCAACCGCTCCCTCTAGTGGG
 2850 EAG1 XMA3,
 ProSerValAlaSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
 2882 CCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTGATAGGCGAGGTAGAGAGTTCGTTGAACG
 2889 BALI, 2903 NHEI,

ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
 1742 GTGGCTGCCAGCTCGCCGCCCGGGTGGCGCTACTGCCTTTGTGGGCGCTGGCTTAGCT
 CACCGACGGGTGCGAGCGCGGGGGGCCACGGCGATGACGAAACACCCGCGACATCGA
 1794 ESPI,
 GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
 1802 GGGCGCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCATAGACATCCTTGCAAGGTAT
 CGCGGGCGGTAGCCGTACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCAT
 1802 KAS1 NARI,
 GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
 1862 GGGCGGGCGGTGGCGGGAGCTCTTTGTGGCATTCAGATCATGAGCGGTGAGGTCCCTCC
 CGCGCCCGCGACCCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
 1878 SACI, 1899 BSPH1,
 ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
 TGCCTCCTGGACCACTTAGATGACGGGCGGTAGGAGAGCGGGCTCGGAGCATCAGCCG
 1928 TTH3I,
 ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
 1982 GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGCGAGTGCAGTGG
 CACCAGACACGTGCTTATGACGCGGCCGTGCAACCGGGGCCGCTCCCCGTCACGTACCC
 2004 NAEI, 2017 SMAI XMAI,
 MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
 2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTACGTG
 TACTTGCCCGACTATCGGAAGCGGAGGGGCCCTTGGTACAAGGGGTGCGTGATGCAC
 2067 SMAI XMAI, 2093 DRA3,
 ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
 2102 CCGGAGAGCGATGACAGCTGCCCGCGTCACTGCCATACTCAGCAGCTCACTGAACCCAG
 GGCTCTCGCTACGTCGACGGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
 2115 PVU2, 2159 ALWN1,
 LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
 2162 CTCTGAGGCGACTGCACCACTGGATAAGCTCGGAGTGTAACCACTCCATGCTCCGGTTCC
 GAGGACTCCGCTGACGTGGTCACCTATTTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
 2164 MST2, 2220 ECON1,
 TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
 2222 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
 ACCGATTCCCTGTAGACCTGACCTATACGCTCCACAACCTCGCTGAATTTCTGGACCGAT
 LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
 2282 AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCTTTGTGTCTGCCAGCGCGGGTAT
 TTTCGATTTCGAGTACGGTGTGACGCGGACCTAGGGGAAACACAGGACGGTCCGCCCAT
 2285 ESPI, 2300 PVU2, 2310 BAMHI,

ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
 2942 ACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCTATGGAGGCAG
 TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
 2966 ESP1, 2969 SACI,
 GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
 3002 GAGATGGGCGGCAACATCACCAGGTTGAGTCAGAAAACAAGTGGTGATTCTGGACTCC
 CTCTACCCGCCCTTTAGTAGTGGTCCCACTCAGTCTTTTGTTCACCACTAAGACCTGAGG
 PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 3062 TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCTG
 AAGCTAGCGCAACACCGCTCTCTGCTGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
 3096 BGL2,
 ArgLysSerArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
 3122 CGGAAGTCTCGGAGATTTCGCCCAGGCCCTGCCCGTTTGGGCGCGCCGGACTATAACCC
 GCCTTCAGAGCCTCTAAGCGGGTCCGGACGGGCAACCCGCGCGCTGATATTGGGG
 3143 ALWN1, 3164 EAG1 XMA3,
 ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
 3182 CCGCTAGTGGAGAGCTGGAAAAAGCCCGACTACGAACCACTGTGGTCCATGGCTGCCCG
 GCGCATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAAGTACCGACGGG
 3217 HGIE2, 3229 NCOI,
 LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
 3242 CTTCCACCTCCAAAGTCCCTCCTGTGCCTCCGCCTCGGAAGAGCGGACGGTGGTCCCTC
 GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACAGGAG
 ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
 3302 ACTGAATCAACCTATCTACTGCCTTGGCCGAGCTCGCCACCAAGCTTTGGCAGCTCC
 TGACTTAGTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
 3332 SACI, 3346 HIND3,
 SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
 3362 TCAACTTCCGGCATTACGGGCGACAATACGACAACATCTCTGAGCCCGCCCTTCTGGC
 AGTTGAAGGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCG
 CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
 3422 TGCCCCCGGACTCCGACGCTGAGTCTTCTCTCCATGCCCCCCCTGGAGGGGGAGCCT
 ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
 3437 EAM11051,
 GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
 3482 GGGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
 CCCCTAGGCCTAGAATCGCTGCCAGTACCAGTGGCAGTCATCACTCCGGTTGCCCTC
 3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
 AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
 3542 GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC
 CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG

2342 LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
 AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
 TCCCCCAGACCGCTCCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG

2402 ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCTTAGGACCTGCAGGAACATC
 TGACCTGTACAGTTTTTGCCTGTACTCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,

2462 TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
 TGGAGTGGGACCTTCCCATTAATGCCTACACACGGGGCCCTGTACCCCCCTTCTCGG
 ACCTCACCTCGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGAAGGACGC
 2480 ASE1, 2497 APAI,

2522 ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGAAGCGGATACCTCCACAGACGTCCTCTATGCACCTCTATTCCGTC
 2553 PSTI,

2582 ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAACTCTAAATGCCCGTGCCAC
 CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTACGGGCACGGTC
 2594 DRA3,

2642 ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
 GTCCCATCGCCCGAATTTTACAGAAATTGGACGGGGTGCCTACATAGGTTTGCGCC
 CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCACCGCGGATGTATCCAAACGCGGG

2702 ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTACAGTAGGACTCCACGAATACCCG
 GGGACGTTCCGGAACGACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTTATGGGC
 2757 HGIE2,

2762 ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
 CATCCAGCGTTAATGGAACGCTCGGGCTTGGCTTGACCGGCACAACTGCAGGTACGAG
 2809 AAT2,

2822 ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 ACTGATCCCTCCCATATAACAGCAGAGGGCGGGCGAAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGGTATATTGTCGTCTCCGCGGGCCGCTTCCAACCGCTCCCTTAGTGGG
 2850 EAG1 XMA3,

2882 ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
 2889 BALI, 2903 NHEI,

- 1742 ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
GTGGCTGCCAGCTCGCCGCCCTCCGGTGGCCGTACTGCCTTTGTGGGCGCTGGCTAGCT
CACCAGCGGTCGAGCGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA
1794 ESP1,
- 1802 GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
GGCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCCTCATAGACATCCTTGAGGGTAT
CCGCGCGGTAGCGCTCACAACTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCTCCATA
1802 KAS1 NARI,
- 1862 GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCCTCC
CCGCGCCCCGACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
1878 SACI, 1899 BSPH1,
- 1922 ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
ACGGAGGACCTGGTCAATCTACTGCCGCCATCTCTCGCCCGGAGCCCTCGTAGTCGGC
TGCCTCTTGACACGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
1928 TTH3I,
- 1982 ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCCGGCGAGGGGCGAGTGCAGTGG
CACCAGACACGCTGTTATGACCGGGCGGTGCAACCGGGCCCCGTCCCCGTACGTCACC
2004 NAEI, 2017 SMAI XMAI,
- 2042 MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTACGTG
TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGTGCGTGATGCAC
2067 SMAI XMAI, 2093 DRA3,
- 2102 ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
CCGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCGTC
GGCCTCTCGTACGTGCAGGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
2115 PVU2, 2159 ALWN1,
- 2162 LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
CTCCTAGGGCGACTGCACCACTGGATAAGCTCGGAGTGTACCACCTCATGTCCGGTTCC
GAGGACTCCGCTGACGTGGTCACTATTTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
2164 MST2, 2220 ECON1,
- 2222 TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
ACCGATTCCCTGTAGACCTTGACCTATACGCTCCACAACCTCGTGAAATTCGAGCCGAT
- 2282 LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCTTTGTGTCTGCCAGCGCGGGTAT
TTTCGATTGAGTACGGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCAT
2285 ESP1, 2300 PVU2, 2310 BAMHI,

TCCCGAGTTCGGGGAGGGGGTAGCACCCCTGGTCTACACCTTCACAACTAAGCGGAGTTC
 ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
 ^
 1150 NCOI,
 ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
 1202 ACCCTGACGCACCCAGTCACCAATACATCATGACATGCATGTGCGCCGACCTGGAGGTC
 TGGGACTGCGTGGGTGAGTGGTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
 ^ ^ ^ ^ ^
 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
 ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGGCTCTGGCTGCTTGGCCGCGATTGCGCTG
 CAGTGCTCGTGACCCACGAGCAACCCCGCAGGACGACGAAACCGGCGCATTAACGGAC
 SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGTCGCTCTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCATATCACCCGTCCCAGCAGAACAGGCCCTTCGGCGCTTAGTAT
 ^
 1369 NAEI,
 ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCAGGAGAGTCGTGAAT
 ^
 1385 DRD1,
 ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAGCAGAAAGCCCTCGGCCCTC
 GGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCGGGAGCCGGAG
 LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGACCGGCTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGGCAGTCCGCTCTCCAATAGCGGGGACGACAGTCTGTTGACCGTT
 ^ ^ ^
 1502 PSTI, 1507 TTH3I,
 LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 1562 AAATCTGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAGAGCCCGCTTCGTATACACCTTGAAGTAGTACCCCTATGTTATGAAC
 ^
 1565 XHOI, 1586 NDEI,
 AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
 1622 CGGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
 CGCCCGAACAGTTGGCAGGCACCATTTGGGGCGGTAAACGAAGTAACACCGAAAATGTGCA
 ^ ^ ^
 1643 BSTE2, 1677 ALWN1 PVU2,
 AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCAACGACCCACTAACCACTAGCCAAACCCCTCTCTCAACATATTGGGGGGGTGG
 CGACAGTGGTGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCACC

FIG. 22–Page 3

SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 482 TCAAAGAAGAAAGTGCAGCAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
 AGTTTCTTCTTCACGTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
 AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCACTCCGACCAGCGCGATGTTGTCTGCTG
 CGGATGATGGCGCCAGAAGTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
 550 SAC2, 560 DRD1,
 AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
 602 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
 CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
 615 BSPH1,
 ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACGTGTGTCAACCCAGACAGTCGATTTTCAGCCTTGACCCTACCTTCACATTGAGACAATC
 TGCACACAGTGGGTCTGTGACGTAAAGTCGGAAGTGGATGGAAGTGGTAACTCTGTTAG
 ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 722 ACGTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
 TGCGAGGGGGTTCACGACAGAGGGCGTGAGTTGCACGCCCTCTGACCGTCCCCCTTC
 ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 782 CCAGGCATCTACAGATTTTGTGGCACCGGGGGAGCGCCCCCTCCGGCATGTCGACTCGTCC
 GGTCCGTAGGTCTAAACACCGTGGCCCCCTCGCGGGGAGCCGTACAAGCTGAGCAGG
 816 BGLI, 833 DRD1,
 ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
 842 GTCCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
 CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGA
 881 SACI,
 ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
 902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
 TGTCATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTCTGGTAGAA
 931 SMAI XMAI,
 GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCACTTTCTATCCAG
 CTTAAACCCCTCCCGCAGAAATGTCGGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
 985 STUI,
 ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
 1022 ACAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
 TGTTTCGCTCACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
 1069 DRA3,
 ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 1082 AGGGCTCAAGCCCCCTCCCCCATCGTGGGACCAGATGTGGAAAGTGTGATTTCGCTCAAG

TCCCAGAGTTCGGGGGAGGGGGTAGCACCCCTGGTCTACACCTTCACAACTAAGCGGAGTTTC
 ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCCTCCATGGGGCAACACCCCTGCTATACAGACTGGGCGCTGTTGAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAGTCTTACTTTAG
 ^
 1150 NCOI,
 ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
 1202 ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTGCGCCGACCTGGAGGTC
 TGGGACTGCGTGGGTGAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
 ^ ^ ^
 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
 ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGCTCTGGCTGCTTTGGCCGCGTATTGCGCTG
 CAGTGCTCGTGGACCCACGAGCAACCGCCGCGAGACCGAGCAACCGGCGCATAAACGGAC
 SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCAATATCACCCGTCCCAGCAGAAACAGGCCCTTCGGCCGTTAGTAT
 ^
 1369 NAEI,
 ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCAGGAGAGTCGTGAAT
 ^
 1385 DRD1,
 ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAGGAGAGGAGCCCTCGGCCCTC
 GGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCGGGAGCGCGGAG
 LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGGGAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGTTGACCGTT
 ^ ^
 1502 PSTI, 1507 TTH3I,
 LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 1562 AAATCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTACCCCTATGTTATGAAC
 ^ ^
 1565 XHOI, 1586 NDEI,
 AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
 1622 CGGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
 CGCCCGAACAGTTGCGACGGACATTGGGGCGGTAACGAAGTAACACCGAAATGTGCGA
 ^ ^ ^
 1643 BSTE2, 1677 ALWN1 PVU2,
 AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCAACAGCCCACTAACCACTAGCCAAACCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTCCGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCACC

TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTCGTCGCCGC

3782 SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
TCAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGACGCTGACGCCCCACAC
AGTTTTCACCTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
3816 HIND3,

3842 SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAGACGTCGGTGGCCATGCCAGAAAGGCC
AGTCGGTTTAGGTTCAAACCAATACCCGTTTTCTGCAAGGCAACGGTACGGTCTTTCCGG
3875 AAT2, 3890 BGLI,

3902 ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACCAATAGAC
CATTTGGGTGATGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG

3962 ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGTTCGTAAG
TGATGGTAGTACCGATTCTTGCTCCAAAGACGCAAGTCGGACTCTTCCCCCAGCATTC

4022 ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
CCAGCTCGTCTCATCGTGTTCGCCGATCTGGCGTGCAGCTGTGCGAAAAGATGGCTTTG
GGTGCAGCAGAGTAGCACAAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC

4082 TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
TAGCAGCTGGTTACAAAGCTCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
ATGCTGCAACCAATGTTTCGAGGGGAACCGGCACTACCTTCGAGGTGCGCTAAGGTTATG

4142 SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
TCACAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGAAGTCCAAGAAAACCCCAATG
AGTGGTCTGTGCGCCAACTTAAGGAGCACGTTTCGACCTTCAGGTTCTTTTGGGGTTAC
4160 ECORI,

4202 GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
GGGTTCTCGTATGATACCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
CCCAAGAGCATACTATGGGCGACGAACTGAGGTGTCAGTGACTCTCGCTGATGGCATGC
4229 DRD1, 4236 ALWN1,

4262 GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCTGGCCATCAAGTCC
CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCCGGGCGCAACCGGTAGTTCAGG
4301 BGLI, 4308 BALI,

4322 LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAATCGCGG
GAGTGGCTCTCCGAAATACAACCCCGGGAGAATGGTTAAGTTCCCCCTCTTGACGCCG
4345 APAI,

4382 TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
TATCGCAGGTGCCGCGAGCGGCGTACTGACAACCTAGCTGTGGTAACACCCCTCACTTGC
ATAGCGTCCACGGGCGCTCGCCGCATGACTGTTGATCGACACCATTTGTGGGAGTGAACG

SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 482 TCAAAGAAGAAGTGGCAGCAACTCGCCGCAAGCTGGTTCGATTGGGCATCAATGCCGTG
 AGTTTCTTCTTACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGATAGTTACGGCAC

AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
 542 GCCTACTACCGGGCTTGTGACGTGTCCGTATCCCGACCAGCGGCATGTTGTCGTCGTG
 CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCCCGCTACACAGCAGCAC
 550 SAC2, 560 DRD1,

AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
 602 GCAACCGATGCCCTCATGACCGGCTATACCGCGCACTTCGACTCGGTGATAGACTGCAAT
 CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
 615 BSPH1,

ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACGTGTGTACCCAGACAGTCGATTTCAGCCTTGACCTACCTTACCATTGAGACAATC
 TGCACACAGTGGGTCTGCAGCTAAAGTCGGAACCTGGGATGGAAAGTGGTAACCTCTGTTAG

ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 722 ACGTCTCCCCAAGATGCTGTCTCCCGCACTCAACGCTCGGGCAGGACTGGCAGGGGGAAG
 TGGCAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCCGTCCTCCCTTC

ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 782 CCAGGCATCTACAGATTGTGGCACCAGGGGAGCGCCCTCCGGCATGTTGCACTCGTCC
 GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGGCGTACAAGCTGAGCAGG
 816 BGLI, 833 DRD1,

ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
 842 GTCTCTGTGAGTGCTATGACGCAAGGCTGTGCTTGGTATGAGCTACGCCCCGCCGAGACT
 CAGGAGACACTCACGATACTGCGTCCGACACGAACCATATCTCGAGTGGCGGCGGCTCTGA
 881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
 902 ACAGTTAGGCTACGAGCGGTACATGAACACCCCGGGGCTTCCGCTGTGCCAGGACCATCTT
 TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTCTGGTAGAA
 931 SMAI XMAI,

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCGAG
 CTTAAACCCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
 985 STUI,

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
 1022 ACAAGCAGAGTGGGAGAACCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
 TGTTTCGTCTACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGGTGCCACACGCGA
 1069 DRA3,

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 1082 AGGGCTCAAGCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTGTTGATTCGCCTCAAG

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
 2 AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
 TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATATCCACGATCATGAGTTG
 ^ ^ ^
 1 HIND3, 24 NDEI, 52 SCAI,
 ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62 CCCTCTGTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
 GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
 ^
 116 CLAI,
 ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGGTGAGAACAAATTACCACTGGCAGCCCCATCAGTACTCCACC
 GGATTGTAGTCTCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
 TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 182 TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGCGCTTATGACATAATAATTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGGAATACTGTATTATTAAACG
 AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCTTGACCAA
 CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCTAACCGTGACAGAACTGGTT
 AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 302 GCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCACCGACCCCTCCGGGCTCCGTC
 CGTCTCTGACGCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGAGGAGCAG
 ^
 303 ALWN1,
 ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 362 ACTGTGCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGAGAGATCCCTTTT
 TGACACGGGGTAGGGTTGTAGTCTCTCCAACGAGACAGGTGGTGGCCCTCTCTAGGGAAAA
 TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 422 TAGGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTGCAT
 ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCTCTGTAGAGTAGAAGACAGTA

FIG. 22-Page 1

5449 APAI,

5462 GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTTCGCAACCTCGAGGTAGACGTCAGCCT
 CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
 ^ ^ ^ ^ ^

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

5522 IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 ATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCCTTGGCCC
 TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGGCCATGGGAACCGGG
 ^ ^ ^ ^ ^

5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

5582 LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCGTGGCTCTCGG
 GAGATACCGTTACTCCGACGCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

5642 ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAsp
 CCTAGCTGGGGCCCCACAGACCCCGCGGTAGGTCGCGCAATTTGGGTAAAGTCATCGAT
 GGATCGACCCCGGGGTGCTGCGGGCCGCATCCAGCGCGTTAAACCATTCAGTAGCTA
 ^ ^ ^

5650 APAI, 5696 CLAI,

5702 ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValOC AM
 ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCTAATAGTCGAC
 TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGATTATCAGCTG
 ^ ^ ^

5724 HGIE2, 5755 SALI,

FIG. 21-Page 10

3122 CGGAAGTCTCGGAGATTGCGCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
 GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCCCGGCCCTGATATTGGGG
 3143 ALWN1, 3164 EAG1 XMA3,
 ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
 3182 CCGCTAGTGGAGAGCTGGAAAAAGCCCGACTACGAACCACTGTGGTCCATGGCTGCCCG
 GCGCATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGACACAGGATACCGACGGCG
 3217 HGIE2, 3229 NCOI,
 LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
 3242 CTTCACCTCCAAAGTCCCTCCTGTGCTCCGCCCTCGGAAGAAGCGGACGCTGGTCCCTC
 GAAGGTGGAGGTTTCAGGGGAGGACACGGAGCGGAGCCTTCTTCGGCTGCCACGAGGAG
 ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
 3302 ACTGAATCAACCCTATCTACTGCTTGGCCGAGCTCGCCACAGAAAGCTTTGGCAGCTCC
 TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
 3332 SAC1, 3346 HIND3,
 SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
 3362 TCAACTTCCGGCATTACGGGCGCAATACGACAACATCCTCTGAGCCCCGCCCTTCTGGC
 AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTGAGCGGAGGAAGACCGG
 CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
 3422 TGCCCCCCCCGACTCCGACGCTGAGTCTATTCTCCATGCCCCCCTGGAGGGGGAGCCT
 ACGGGGGGGTGAAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
 3437 EAM11051,
 GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
 3482 GGGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
 CCCCTAGGCCTAGAATCGCTGCCAGTACCAAGTTGCCAGTCATCACTCCGGTTGCGCCTC
 3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
 AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
 3542 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCGTCGCGCC
 CTACAGCACACGACGAGTTACAGAARTGAGAACCTGTCCGCTGAGCAGTGGGGCACCGCG
 3589 DRA3, 3600 SAC2,
 AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
 3602 CGGAAGAACAGAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
 CGCCTTCTTGTCTTTGACGGGTAGTTACGTATTGCTTGGACACGATGCAAGTGGTGTTA
 3611 ALWN1, 3655 PFLM1,
 LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
 3662 TTGGTGTATTCCACCACCTCAGCAGTGCTTGCCAAAGGCAGAGAAAGTACATTGAC
 AACCACATAAGGTGGTGGAGTCGCTCACGAACGGTTTCCGCTCTTCTTTCAGTGTAAGTCTG
 3681 DRA3,
 ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
 3722 AGACTGCAAGTTCTGGACAGCCATTACAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG

FIG. 18—Page 6

2522 ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 CCGAACTACACGTTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGCAAGCGGATACCTCCACAGACGTCCTCTTATGCACCTCTATTCCGTC
 2553 PSTI,
 ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
 2582 GTGGGGGACTTCCACTACGTACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
 CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
 2594 DRA3,
 ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
 2642 GTCCCATCGCCGAATTTTTCACAGAATTGGACGGGGTGGCGCTACATAGGTTTGGCGCC
 CAGGGTAGCGGGCTTAAAGTGTCTTAACCTGCCCGACGGGATGTATCCAAACGGGG
 ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTAGAGTAGGACTCCACGAATACCCG
 GGGACGTTCCGGGAACGACGCCCTCCTCATAGTAAGTCTCATCTGAGGTGCTTATGGGC
 2757 HGIE2,
 ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCGGTGTTGACGTCCATGCTC
 CATCCAGCGTTAATGGAACGCTCGGGCTTGGCTGCACCGGCACAACCTGCAGGTACGAG
 2809 AAT2,
 ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCGGGCGAAGGTTGGCGAGGGGATACCC
 TGACTAGGAGGGTATATTGTCGTCTCCGCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
 2850 EAG1 XMA3,
 ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
 2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTTCGAGGAGCCGATCGGTTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
 2889 BALI, 2903 NHEI,
 ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
 2942 ACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCTATGGAGGCAG
 TGCGGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGTTGGAGGATACCTCCGTC
 2966 ESP1, 2969 SACI,
 GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
 3002 GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAAACAAAGTGGTGATTCTGGACTCC
 CTCTACCGCGGTTGTAGTGGTCCCACTCAGTCTTTTGTTCACCACTAAGACCTGAGG
 PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 3062 TTCGATCCGCTTGTTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCCGAGAAATCCTG
 AAGCTAGGCGAACACCGCTCCTCTGCTCGCCCTCTAGAGGATGGGCGTCTTAGGAC
 3096 BGL2,
 ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
2 AGCTTACAAAACAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
TCGAATGTTTTTGGTTTACCGACGTATACGTCGAGTCCCATATTCCACGATCATGAGTTG
^ ^ ^
1 HIND3, 24 NDEI, 52 SCAI,

ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
62 CCCTCTGTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
^
116 CLAI,

ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
122 CCTAACATCAGGACCGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGATGAGGTGG

TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleCys
182 TACGCCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGCGCTTATGACATAATAATTTGT
ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGCAATACTGTATTATTAAACA

AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGCTCCTTGACCAA
CTGCTCACGGTGAGGTGCCTACGGTGAGGTAGAACCCTAACCCTGACAGGAATCGGTT

AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
302 GCAGAGACTCGGGGGCGAGACTGGTGTGTGCTCGCCACGCCACCCCTCCGGGCTCCGTC
CGTCTCTGACGCCCGGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGAGGCAG
^
303 ALWN1,

ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
362 ACTGTGCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
TGACACGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGA

TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
422 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTCAT
ATGCCGTTCCGATAGGGGAGCTTCATTAGTTCCCCCTCTGTAGAGTAGAAGACAGTA

FIG. 21-Page 1

4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
 TCCCTGGTGCAACTTGTCCGGGAGCTAACGCTCTAGATGCCCGGACGATGAGGTATCTT
 4893 BGL2,

ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
 4922 CCATGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTCCTACTCCAC
 GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
 4954 NCOI,

SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
 4982 AGTTACTCTCCAGGTGAAATCAATAGGTTGGCCGCATGCCTCAGAAAACCTTGGGGTACCG
 TCAATGAGAGGTCCACTTTAGTTATCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
 5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
 5042 CCCTTGCAGGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
 GGGAAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCATCCGAAGACCGGCTCTCT
 5064 APAI, 5091 BALI,

GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCACTGGGCAGTAAGAACAAAGCTCAAA
 CCGTCCCGACGGTATACACCGTTCTAGGAGAAGTTGACCGCTATTCTTGTTTCGAGTTT
 5113 NDEI,

LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
 5162 CTCCTCCATAGCGGGCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
 GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
 5174 NOTI, 5175 EAGI XMA3, 5182 BALI, 5186 PVU2,

SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
 5222 AGCGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGGCCCGCTGGATCTGGTTTTCG
 TCGCCCCCTCTGTAATAGTGTGCGACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
 5240 DRA3,

LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
 5282 CTACTCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCAGCAAT
 GATGAGGACGAACGACGTCCCATCCGTAGATGGAGGAGGGGTGGCTTACTCGTGCTTA
 5295 PSTI,

ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
 5342 CCTAAACCTCAAAGAAAGACCAACGTAACACCAACCGGCGGCGCAGGACGTCAAGTTC
 GGATTGGAGTTTCTTCTGGTTTGCAATTGTGGTTGGCCGCGCGCTCCTGCAGTTCAAG
 5380 NOTI, 5381 EAGI XMA3, 5390 AAT2, 5401 SMAI XMAI,

ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
 5402 CCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGGCCCTAGATTG
 GGCCACCGCCAGTCTAGCAACCACTCAAATGAACAACGGCGCTCCCGGGATCTAAC

FIG. 21-Page 9

4229 DRD1, 4236 ALWN1,

4262 GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCTGGCCATCAAGTCC
 CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCCGGCGCACCGGTAGTTCAGG
 ^ ^

4301 BGLI, 4308 BALI,

4322 LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAGCTCGCGC
 GAGTGGCTCTCGAAATACAACCCCGGAGAATGGTTAAGTTCCTCCCTCTTACGCGCG
 ^

4345 APAI,

4382 TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 TATCGCAGGTGCCCGCGAGCGGCGTACTGACAACCTAGCTGTGGTAACACCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTTGTGGGAGTGAACG

4442 TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 TACATCAAGGCCCCGGGACGCTGTCGAGCCGACGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCGGGGCCGTCGGACAGCTCGGCGTCCCGAGGTCTGACGTGGTACGACGAC
 ^

4452 SMAI XMAI,

4502 CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 TGTGGCGACGACTTAGTCGTTATCTGTGAAGCGCGGGGTTCCAGGAGGACGCGCGGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCAGGTCTCTGCGCCGCTCG
 ^ ^

4508 DRD1, 4511 TTH3I,

4562 LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGCGGGGGGACCCCTGGGGGGTGT

4622 ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 CCAGAATACGACTTGGAGCTCATAACATCATGCTCTCCAACGTGTCACTGCCCCACGAC
 GGTCTTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGTTGCACAGTCAGCGGGTGCTG
 ^

4637 SACI,

4682 GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
 GGCGCTGGAAGAGGGTCTACTACCTCACCGGTGACCTACAACCCCTCGCGAGAGCT
 CCGGACCTTTCTCCAGATGATGGAGTGGGCACTGGGATGTGGGGGGAGCGCTCTCGA
 ^

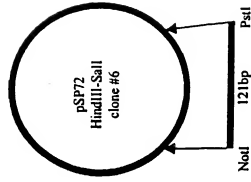
4731 NRUI,

4742 AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 CGCTGGGAGACAGCAAGACACACTCCAGTCAATTCTGGCTAGGCAACATAATCATGTTT
 CGCACCTCTGTGCTTCTGTGTGAGGTCAAGTAAAGACCGATCCGTTGTATTAGTACAAA

4802 AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
 GCCCCACACTGTGGGCGAGGATGATACTGATGACCATTTCTTTAGCGTCTTTATAGCC
 CGGGGGTGTGACACCCGCTCTACTATGACTACTGGTAAAGAAATCGCAGGAATATCGG
 ^ ^

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu



Ligate fragments into pd.ΔNS3NS5.PJ
NdeI-Sall cloning vector.

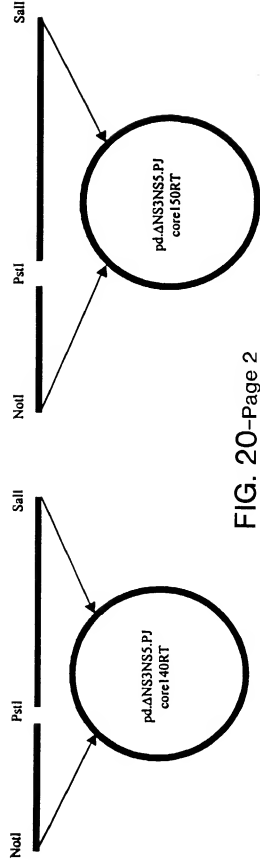


FIG. 20-Page 2

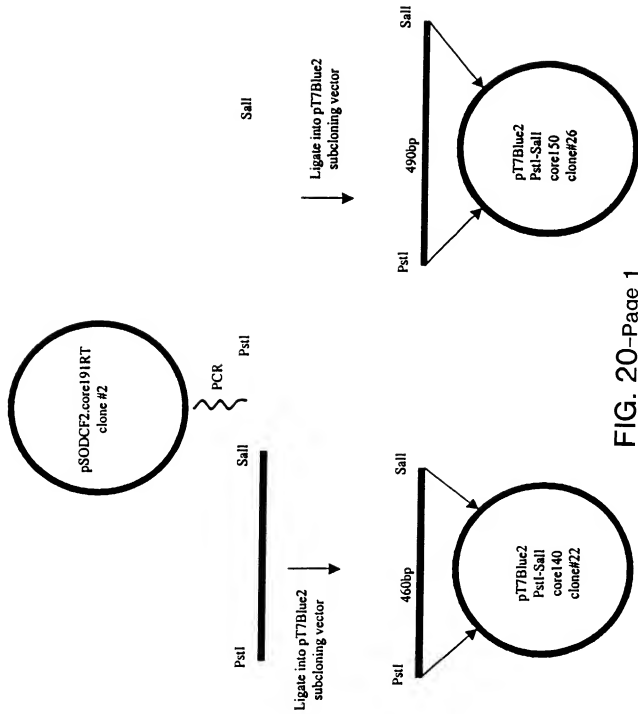


FIG. 20-Page 1

1922 ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
ACGGAGGACCTGGTCAATCTACTGCCCGCATCCTTCGCCCCGAGCCCTCGTAGTCGGC
TGCTCTCTGGACCACTTAGATGACGGGCGGTAGGAGAGCGGCCTCGGGAGCATCAGCCG
1928 TTH3I,
ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
1982 GTGGTCTGTGCAGCAATACTGCGCCGGCAGCTTGGCCCCGGGAGGGGGCAGTGCAGTGG
CACCAGACACGTCGTTATGACGCGCCGTGCAACCGGGCCCGCTCCCCGTCACGTCAAC
2004 NAEI, 2017 SMAI XMAI,
MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCACGCACTACGTG
TACTTGGCCACTATCGGAAGCGGAGGGCCCCCTTGGTACAAGGGGGTGCCTGATGCAC
2067 SMAI XMAI, 2093 DRA3,
ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
2102 CCGGAGAGCGATGACGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
2115 PVU2, 2159 ALWN1,
LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
2162 CTCCTGAGGCCACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
GAGGACTCCGCTGACGTGGTCACCTATTTCGAGCTCACATGGTGAGGTACGAGGGCAAGG
2164 MST2, 2220 ECON1,
TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
2222 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGGCTA
ACCGATTCCCTGTAGACCCCTGACCTATACGCTCCACAACCTCGCTGAAATCTGGACCCGAT
2282 LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCCTTGTGTCCTGCCAGCGCGGGTAT
TTTCGATTTCGAGTACGGTGTGACGGACCCCTAGGGGAAACACAGGACGGTCGCGCCCAT
2285 ESP1, 2300 PVU2, 2310 BAMHI,
LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
2342 AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
TTCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
2402 ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCTAGGACCTGCAGGAACATG
TGACCTGTACAGTTTTTGGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCTGTACCCCCCTTCTCGCG
ACCTCACCTTGAAGGGGTAAATTACGGATGTGGTCCCCGGGGACATGGGGGGAAGGACG
2480 ASE1, 2497 APAI,

FIG. 18-Page 4

CAGTGCTCGTGGACCCACGAGCAACCGCCGAGGACCGACGAAACCGGCGCATAACGGAC
 SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTCGTGGTTCATAGTGGGCAAGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCATGATACACCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
 1369 NAEI,
 ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAAGTCCCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAAT
 1385 DRD1,
 ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCCTC
 GGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
 LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 LCCAGACCCGCTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT
 1502 PSTI, 1507 TTH3I,
 LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 1562 AAACCTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTACCCCTATGTTATGAAC
 1565 XHOI, 1586 NDEI,
 AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
 1622 GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
 CGCCCGAACAGTTGGCAGCGACCATTTGGGGCGGTAAACGAAGTAACACCGAAAAATGTCGA
 1643 BSTE2, 1677 ALWN1 PVU2,
 AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTACACGAGCCCATACCACTAGCCAAACCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCACC
 ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
 1742 GTGGCTGCCAGCTCGCCGCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCT
 CACCGACGGTTCGAGCGGGGGGCCACGGCGATGACGGAACACCCGCGACCGAATCGA
 1794 ESP1,
 GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
 1802 GCGCGGCCCATCGGCAGTGTGGACTGGGGAAGTCCCTCATAGACATCCTTGCAGGGTAT
 CCGCGCGGTAGCCGTACAACTGACCCTTCCAGGAGTATCTGTAGGAACGTCCCAT
 1802 KAS1 NARI,
 GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
 1862 GCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCCTCC
 CGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
 1878 SACI, 1899 BSPH1,

LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
 2342 AAGGGGGTCTGGCGAGGGGACGGGCATCATGCACACTCGTGCCACTGTGGAGCTGAGATC
 TTCCCCAGACCGCTCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
 ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
 2402 ACTGGACATGTCAAAACGGGACGATGAGGATCGTCGGTCTTAGGACCTGCAGGAACATG
 TGACCTGTACAGTTTTTGCCCTGCTACTCTTAGCAGCCAGGATCCTGGACGCTCTTGATC
 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
 TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
 2462 TGGAGTGGGACCTTCCCCATTAAATGCCTACACCACGGGCCCCCTGTACCCCCCTTCCTGCG
 ACCTCACCTCGGAAGGGTAATTACGGATGTGGTGCCCGGGACATGGGGGGAAGGACGC
 2480 ASE1, 2497 APA1,
 ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 2522 CCGAATACACGTTGCGCTATGGAGGGTGCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGCAAGCGCGATACCTCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
 2553 PSTI,
 ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
 CACCCCCGAAGGTGATGCACTGCCCATCTGATGACTGTTAGAAATTTACGGGCACGGTC
 2594 DRA3,
 ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
 2642 GTCCCATCGCCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC
 CAGGGTAGCGGGGCTTAAAGTGCTTAACTGCCACCGCGGATGTATCCAAACGCGGG
 ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTGAGTAGGACTCCACGAATACCCG
 GGGACGTTGCGGAACGACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTTATGGGC
 2757 HGIE2,
 ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
 CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACCTGACGGTACGAG
 2809 AAT2,
 ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGCGAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGTATATTGTCGTCTCCGCGGCCCGCTTCCAACCGCTCCCTTAGTGGG
 2850 EAG1 XMA3,
 ProSerValAlaSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
 2882 CCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCTGTTGAACG
 2889 BALI, 2903 NHEI,

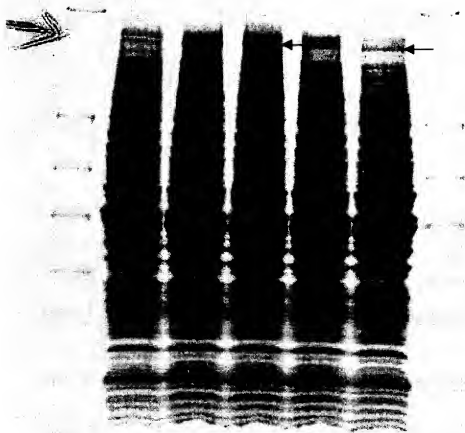


FIG. 19

ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
 1742 GTGGCTGCCAGCTCGCCGCCCGCGTGGCGCTACTGCCTTTGTGGCGCTGGCTTAGCT
 CACCGACGGGTCGAGCGGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA
 1794 ESPI,
 GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
 1802 GCGCGCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCATAGACATCTTGCAGGGTAT
 CCGCGCGGTAGCCGTACAACTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATATA
 1802 KASI NARI,
 GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
 1862 GCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGTCCCTCC
 CCGCGCCCGCACCCGCCCTCGAAGACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
 1878 SACI, 1899 BSPH1,
 ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
 TGCCTCTGGACCACTTAGATGACGGGCGGTAGGAGAGCGGGCTCGGGAGCATCAGCCG
 1928 TTH3I,
 ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
 1982 GTGGTCTGTGCAGCAATACTGCGCCGCGCACGTTGGCCCGGGCGAGGGGCGAGTGCAGTGG
 CACCAGACACGTCGTTATGACGCGGCGGTGCAACCGGGCCGCTCCCCCGTCACGTACCC
 2004 NAEI, 2017 SMAI XMAI,
 MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
 2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTACGTG
 TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTGGGTACAAGGGGTGCGTGATGCAC
 2067 SMAI XMAI, 2093 DRA3,
 ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
 2102 CCGGAGAGCGATGACGCTGCCGCGTCACTGCCATACTCAGCAGCTCACTGTAACCCAG
 GGCCTCTCGTACGTGACGGGCGCAGTGACGGTATGAGTCGTGCGAGTGACATTGGGTC
 2115 PVU2, 2159 ALWN1,
 LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProGlySerGlySer
 2162 CTCTGAGGGGACTGCACCACTGGATATGCGAGGTGTGAGCGACTTTAAGACCTGGCTA
 GAGGACTCCGCTGACGTGGTCACCTATTGAGCCCTCACATGGTGAGGTACGAGGCCAAGG
 2164 MST2, 2220 ECON1,
 TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
 2222 TGGCTAAGGACATCTGGGACTGGATATGCGAGGTGTGAGCGACTTTAAGACCTGGCTA
 ACCGATTCCCTGTAGACCTGACCTATACGCTCCACAACCTCGCTGAATTTCTGGACCGAT
 2282 LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
 AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCTTTGTGTCTGCCAGCGCGGGTAT
 TTTTCAGTTCGAGGTGTCGACGGACCTTAGGGGAAACACAGGACGGTGCGCCCATATA
 2285 ESPI, 2300 PVU2, 2310 BAMHI,

TCCCGAGTTCGGGGAGGGGGTAGCACCCCTGGTCTACACCTTCACAACTAAGCGGAGTTC
 ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAAGATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGCTTTACTTTAG
 ^
 1150 NCOI,
 ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
 1202 ACCCTGACGCACCCAGTCACCAATACATCATGACATGCATGTCTGGCCGACCTGGAGGTC
 TGGGACTGCGTGGGTGAGTGTATGTAGTACTGTACGACGCGGCTGGACCTCCAG
 ^ ^ ^ ^ ^
 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
 ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCTCGGTGCTTTGGCCGCGTATTGCCCTG
 CAGTGCTCGTGGACCAACGAGCAACCGCCGAGACGACGAAACCGGCGCATAAACGGAC
 SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
 ^
 1369 NAEI,
 ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CTGACAGCGGAAGTCTCTACCCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCAGCAGAGTCGTGAAT
 ^
 1385 DRD1,
 ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCCTC
 GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCGGGGAGCCGGAG
 LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGCCGCGTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGCGAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT
 ^ ^ ^
 1502 PSTI, 1507 TTH3I,
 LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 1562 AAATCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTACCCCTATGTTATGAAC
 ^
 1565 XHOI, 1586 NDEI,
 AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
 1622 GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
 CGCCCGAACAGTTGCGACGGACCATTTGGGGCGGTAAACGAAGTAACTACCGAAAATGTCGA
 ^ ^ ^
 1643 BSTE2, 1677 ALWN1 PVU2,
 AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCCACGACCCACTAACCCTAGCCAAACCCCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCACC

FIG. 17-Page 3

ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACCTGTGTACCCAGACAGTCGATTTACGCCCTTACCCCTACCTTACCATTGAGACAACT
 TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACCTGGGATGGAAGTGGTAACCTCTGTTAG

ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 722 ACGCTCCCCAAGATGCTGCTCCTCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
 TCGCAGGGGGTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCTGACCGTCCCCCTTC

ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 782 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCTCCGGCATGTTGCGACTCGTCC
 GGTCCGTAGATGCTAAACACCGTGCCCTCGCGGGAGGCCGTACAAGCTGAGCAGG

816 BGLI, 833 DRD1,

ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
 842 GTCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
 CAGGAGACACTCACGATACTCGCTCCGACAGCAACCATACTCGAGTCGGCGCGGCTCTGA

881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
 902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
 TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTCTGGTAGAA

931 SMAI XMAI,

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
 962 GAATTTTGGGAGGGCGCTTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCAG
 CTTAAACCCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC

985 STUI,

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
 1022 ACCAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
 TGTTCGTCTCACCCCTCTTGGGAAGGAATGGACCATCGCATGTTTGGGTGGCACACCGCA

1069 DRA3,

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 1082 AGGGCTCAAGCCCCCTCCCCATCGTGGGACCAGATGTGGAAGTGTGATTGCGCTCAAG
 TCCGAGTTCGGGGAGGGGGTAGCACCTTGGTCTACACCTTACAAACTAAGCGGAGTTTC

ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCACCCCTCCATGGGCCAACACCCCTGTATACAGACTGGCGCTGTTGAGAAATGAAATC
 GGGTGGGAGGTACCCGGTGTGGGGACGATATGCTGACCCCGCACAAGTCTTACTTTAG

1150 NCOI,

ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
 1202 ACCCTGACGCACCCAGTACCAAATACATCATGACATGCTGCGGCCGACCTGGAGGTC
 TGGGACTGCGTGGGTGAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG

1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCTGGCTGCTTTGGCCGCTATTGCGCTG

5642 ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAsp
 CCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
 GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
 ^ ^
 5650 APAI, 5696 CLAI,

 5702 ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
 ACCCTTACGTGCGGCTTCGCGCACCTCATGGGGTACATACCGCTCGTCGGCGCCCTCTT
 TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
 ^ ^ ^
 5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,

 5762 GlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyr
 GGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACAT
 CCTCCGCGACGGTCCCGGGACCGCGTACCGCAGGCCCAAGACCTTCTGCCGCACCTTGATA
 ^ ^ ^
 5772 BSTXI, 5775 APAI,

 5822 AlaThrGlyAsnLeuProGlyCysSerOC AM
 GCAACAGGGAACCTTCCTGGTTGCTCTTAATAGTCGAC
 CGTTGTCCCTTGAAGACCAACGAGAATTATCAGCTG
 ^
 5854 SALI,

FIG. 18—Page 10

5042 ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
 GGAACCGCTCGAACCCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGCTCTCT
 5064 APAI, 5091 BALI,
 5102 GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
 CGGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
 5113 NDEI,
 5162 LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
 CTCACCTCCAATAGCGGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
 GAGTGAGGTTATCGCCGCGACCGGTGACCTGAACAGGCCGAGCAAGTCCGACCGCATG
 5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
 5222 SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
 AGCGGGGGAGACATTTATCAGCGGTGTCTCATGCCGGCCCGGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAATAGTGTGCGACAGAGTACGGGCCGGGGGACCTAGACCAAAACG
 5240 DRA3,
 5282 LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
 CTACTCTGCTTGTGTCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCAGCAAT
 GATGAGGACGAACGACGTCCCATCCGTAGATGGAGGAGGGGTGGCTTACTCGTGCTTA
 5295 PSTI,
 5342 ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
 CCTAAACCTCAAAGAAAGACCAACGTAACACCAACCGGGCCCGCAGGACGTCAAGTTC
 GGATTTGGAGTTTCTTTCTGGTTTGCAATTGTGGTTGGCCCGCGGCTCCTGCAGTTCAG
 5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
 5402 ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
 CCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGGCCCTAGATTG
 GGCCACCGCCAGTCTAGCAACCACTCAAATGAACAACGGCGCGTCCCGGGATCTAAC
 5449 APAI,
 5462 GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTGCAACCTCGAGGTAGACGTGACGCT
 CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCACTCGGA
 5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,
 5522 IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 ATCCCCAAGGCTCGTCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCTTGGCCCC
 TAGGGGTTCGAGCAGCCGGGTCTCCGTCTGGACCGAGTCCGGCCCATGGGAACCGGG
 5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,
 5582 LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGCTCTCCCGTGGCTCTCGG
 GAGATACCGTTACTCCGACGCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
 2 AGCTTACAAAACAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
 TCGAATGTTTGTGTTTACCAGCTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
 ^ ^
 1 HIND3, 24 NDE1, 52 SCA1,
 ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62 CCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
 GGGAGACAACACGAGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCATGCTA
 ^
 116 CLAI,
 ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGGTGAGAACAAATTACCACTGGCAGCCCATCAGTACTCCACC
 GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
 TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleCys
 182 TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGCAATACTGTATTATTAACA
 AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCATGTCCTTGACCAA
 CTGCTCACGGTGAGGTGCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAAGTGGTT
 AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 302 GCAGAGACTCGCGGGGCGAGACTGGTGTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
 CGTCTCTGACGCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGAGGCCGAGGCGAG
 ^
 303 ALWN1,
 ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 362 ACTGTGCCCCATCCCAACATCGAGGAGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
 TGACACGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCCTCTAGGGAAAA
 TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 422 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTGAT
 ATGCCGTTCCGATAGGGGAGCTTCATTAGTTCCCCCCTCTGTAGAGTAGAAGACAGTA
 SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 482 TCAAAGAAGAAGTGCAGCAACTCGCCGCAAGCTGGTTCGATCGGCGATCAATGCCGCTG
 AGTTTCTTCTTACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
 AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCGCGCGATGTTGTGCTGCTG
 CGGATGATGGCCGAGAATGCACAGGCGAGTAGGGCTGGTCGCCGCTACAAACAGCAGCAC
 ^
 550 SAC2, 560 DRD1,
 AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
 602 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
 CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
 ^
 615 BSPH1,

SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 482 TCAAAGAAGAAGTGCAGCAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
 AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCACGTAACCCGTAGTTACGGCAC
 AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
 542 GCCTACTACCGCGTCTTGACGTGTCCTGCATCCCGACCGCGCATGTTGTCGTCGTG
 CGGATGATGGCGCCAGAAGTGCACAGGCAGTAGGGCTGGTCGCCGTACAACAGCAGCAC
 550 SAC2, 560 DRD1,
 AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
 602 GCAACCGATGCCCTCATGACCGGTATACCGCGCACTTCGACTCGGTGATAGACTGCAAT
 CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
 615 BSPH1,
 ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACGTGTGTCAACCCAGACAGTCGATTTTCAGCCTTGACCTACCTTCACCATTTAGACAATC
 TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAAGTGGGATGGAAGTGAACCTCTGTTAG
 ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 722 ACGTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
 TCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC
 ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 782 CCAGGCATCTACGATTTGTGGCACCGGGGAGCGCCCCCTCCGGCATGTTGCACTCGTCC
 GGTCCGTAGATGCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
 816 BGLI, 833 DRD1,
 ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
 842 GTCCTCTGTGAGTGTATGACGCAAGCTGTGCTTGGTATGAGCTACGCCCCCGGAGACT
 CAGGAGACACTACGATACTGCGTCCGACACGAACCATACTCGATGCGGGCGGCTCTGA
 881 SACI,
 ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
 902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
 TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTCTGGTAGAA
 931 SMAI XMAI,
 GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCGAC
 CTTAAACCTTCCCGCAGAAATGTCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
 985 STUI,
 ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
 1022 ACAAGCAGAGTGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
 TGTTTCGTCTCACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGTTGGGCACACGCGA
 1069 DRA3,
 ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 1082 AGGGCTCAAGCCCTCCCCCATCGTGGGACAGATGTGGAAGTGTGTTGATTGCGCTCAAG

2522 CCGAACTACACGTTCCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
GGCTTGATGTGCAAGCGCGATACCTCCACAGACGTCTCCTTATGCACCTCTATTCGGTC
^

2553 PSTI,
^

2582 ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
CACCCTCGAAGGTGATGCACTGCCCTACTGATGACTGTTAGAAATTTACGGGCACGGTC
^

2594 DRA3,
^

2642 ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGTGCGCCTACATAGGTTTGGCGCC
CAGGGTAGCGGGCTTAAAAAGTGCTTTAACCTGCCCCACGCGGATGATCCAAACGCGGG
^

2702 ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
CCCTGCAAGCCCTTGTCTGCGGAGGAGGTATCATTACAGAGTAGGACTCCACGAATACCCG
GGGACGTTGCGGAACGACGCCCTCTCCATAGTAAGTCTCATCTGAGGTGCTTATGGGC
^

2757 HGIE2,
^

2762 ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
GTAGGGTCGCAATTACCTTGCAGAGCCGAACCGGACGTGGCCGTGTTGAGCTCCATGCTC
CATCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAATGCAGGTACGAG
^

2809 AAT2,
^

2822 ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
ACTGATCCCTCCCATATAACAGCAGAGCGGCGGGCGAAGGTTGGCGAGGGGATCACCC
TGACTAGGAGGGTATATTTGTCGTCTCCGCGCGCCGCTTCCAACCGCTCCCTAGTGGG
^

2850 EAG1 XMA3,
^

2882 ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
GGGAGACACCGGTCGAGGAGCCGATCGGTTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
^

2889 BALI, 2903 NHEI,
^

2942 ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
ACCGTAACCATGACTCCCTGATGCTGAGCTCATAGAGCCAACTCCTATGGAGGCAG
TGGCGATTGTTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGAGGATACCTCCGTC
^ ^

2966 ESP1, 2969 SACI,
^

3002 GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGTTGATTCTGGACTCC
CTCTACCGCGGTTGTAGTGGTCCCACTCAGTCTTTTGTTCACCACTAAGACCTGAGG
^

3062 PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
TTCGATCCGCTTGTGGCGAGGAGGACGAGCGGAGATCTCCGTACCGCGAGAACTCTG
AAGCTAGGCGAACACCGCCTCTCTCTGCTGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
^

3096 BGL2,
^

3122 ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
CGGAAGTCTCGGAGATTCGCCAGGCCCTGCCCGTTTGGGCGCGCGCGGACTATACCCC

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
 2 AGCTTACAAAAACAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
 TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
 ^ ^
 1 HIND3, 24 NDEI, 52 SCAI,
 ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62 CCCTCTGTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
 GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
 ^
 116 CLAI,
 ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGTGAGAACAAATTACCACTGGCAGCCCCATCAGTACTCCACC
 GGATTGTAGTCTCGGCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGATGAGGTGG
 TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 182 TACGGCAAGTTCTTGGCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGCGAATACTGTATTATTAAACA
 AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 242 GACGAGTGCCTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCTTGACCAA
 CTGCTCAGGTTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACCTGGTT
 AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 302 GCAGAGACTGCGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
 CGTCTCTGACGCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGAGGCAG
 ^
 303 ALWN1,
 ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 362 ACTGTGCCCATCCCAACATCGAGGAGGTGCTCTGTCCACACCGGAGAGATCCCTTTT
 TGACACGGGGTAGGGTTGTAGCTCCTCCAACGACAGGTGGTGGCTCTCTAGGGA
 TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 422 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTGCAT
 ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCTCTGTGAGAGTAGAAGACAGTA

FIG. 17-Page 1

TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 4442 TACATCAAGGCCCGGGCAGCCTTGTGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGCCCGCTCGGACAGCTCGGCGTCCCGAGGTCTGACGTGGTACGAGCAC
 ^
 4452 SMAI XMAI,
 CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGCAGACTTAGTCTGTTATCTGTAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCTCTGCGCGCTCG
 ^
 4508 DRD1, 4511 TTH3I,
 LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCTCCGATACCTGGTCCATGAGCGGGGGGACCCCTGGGGGGTGT
 ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCTCTCCAACGTGTGAGTCGCCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGTCTG
 ^
 4637 SACI,
 GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
 4682 GCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCTACAACCCCCCTCGCGAGAGCT
 CCGCGACCTTTCTCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA
 ^
 4731 NRUI,
 AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 4742 GCGTGGGAGACAGACACACTCCAGTCAATTCTCGGTAGGCAACATAATCATGTTT
 CGCACCCCTCTGTCGTTCTGTGTAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
 AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
 4802 GCCCCACACTGTGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
 CGGGGGTGTGACACCCGCTCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
 ^^
 4806 PFLM1, 4807 DRA3,
 ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu
 4862 AGGGACAGCTTGAACAGGCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
 TCCTTGTTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCGGACGATGAGGTATCTT
 ^
 4893 BGL2,
 ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
 4922 CCCTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
 GGTGACCTAGATGGAGGTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAGATGAGGTG
 ^
 4954 NCOI,
 SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
 4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACCTGGGGTACCG
 TCAATGAGAGGTCCACTTTAGTTATCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
 ^ ^
 5015 SPHI, 5035 KPNI,

FIG. 18-Page 8

5449 APAI,

5462 GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGACGTGAGCCT
 CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
 ^ ^ ^

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

5522 IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 ATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGCCCC
 TAGGGGTTCGAGCAGCCGGGCTCCCGTCTGGACCCGAGTCGGGCCCATGGGAACCGG
 ^ ^ ^

5548 ALWN1, 5558 ESPI, 5564 SMAI XMAI, 5568 KPNI,

5582 LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCGTGCTCTCGG
 GAGATACCGTTACTCCCGACGCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

5642 ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysOC AM
 CCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCGCGCAATTGGGTAAGTAATAGTCG
 GGATCGACCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCTATTATCAGC
 ^

5650 APAI, 5698 SALI,

5702 AC
 TG

FIG. 17-Page 10

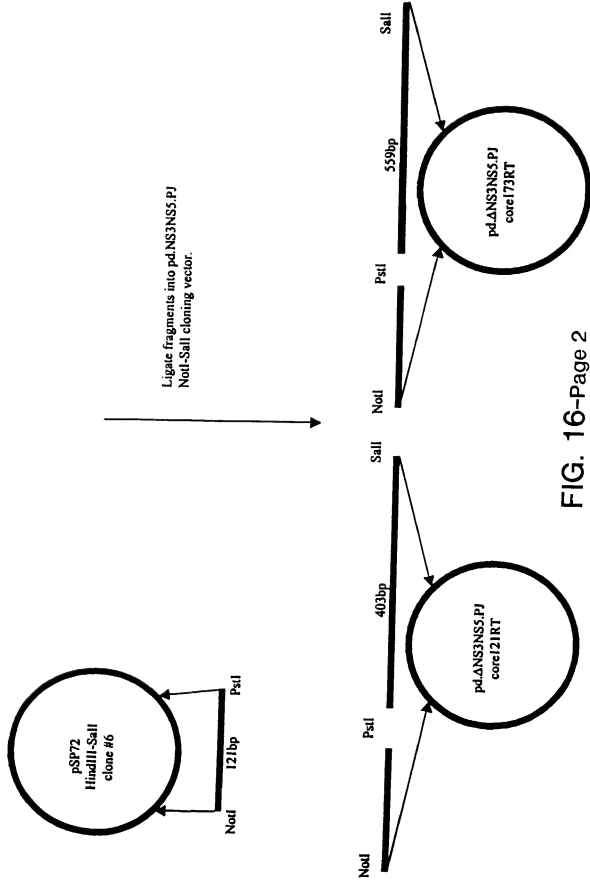


FIG. 16-Page 2

1322 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
TCCTTGGTGAACCTTGTCCGGAGCTAACGCTCTAGATGCCCGGACGATGAGGTATCTT

4893 BGL2,

1382 ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAGTGAGGTG

4954 NCOI,

1442 SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACCTTGGGGTACCG
TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

1502 ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGGAGCTTGGAGACACCGGGCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCATCCGAAGACCGGTCTCCT

5064 APAI, 5091 BALI,

1562 GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GSCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAGCTCAAA
CCGTCGCCGACGGTATACACCGTTTATGGAGAGTTGACCCGTCATTCTTGTTCGAGTTT

5113 NDEI,

1622 LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162 CTCACTCCAATAGCGGGCGCTGGCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
GAGTGAGGTTATCGCCGGCGACCGGTGACCTGAACAGGCCGACCAAGTGGCCAGCCGATG

5174 NOTI, 5175 EAGI XMA3, 5182 BALI, 5186 PVU2,

1682 SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCGGCCCCGCTGGATCTGGTTTTGC
TGGCCCCCTCTGTAAATAGTGTGSCACAGAGTACGGGCGGGGCGACCTAGACAAAACG

5240 DRA3,

1742 LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282 CTACTCTGCTTGTCTGCAGGGGTAGGCATCTACCTCCTCCCAACCGAATGAGCAGCAAT
GATGAGGACGAACGACGTCCCCTCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA

5295 PSTI,

1802 ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342 CCTAAACCTCAAAGAAAGACCAACGTAACCAACCGGCGCCGAGGACGTCAAGTTTC
GGAATTGGAGTTTCTTCTGTTTGCAATGTGGTTGGCCGCGCGGCTCTGCAGTTCAAG

5380 NOTI, 5381 EAGI XMA3, 5390 AAT2, 5401 SMAI XMAI,

1862 ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402 CCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGGCCCTAGATTG
GGCCACCGCCAGTCTAGCAACCACTCAATGAACAACGGCGCGTCCCGGGATCTAAC

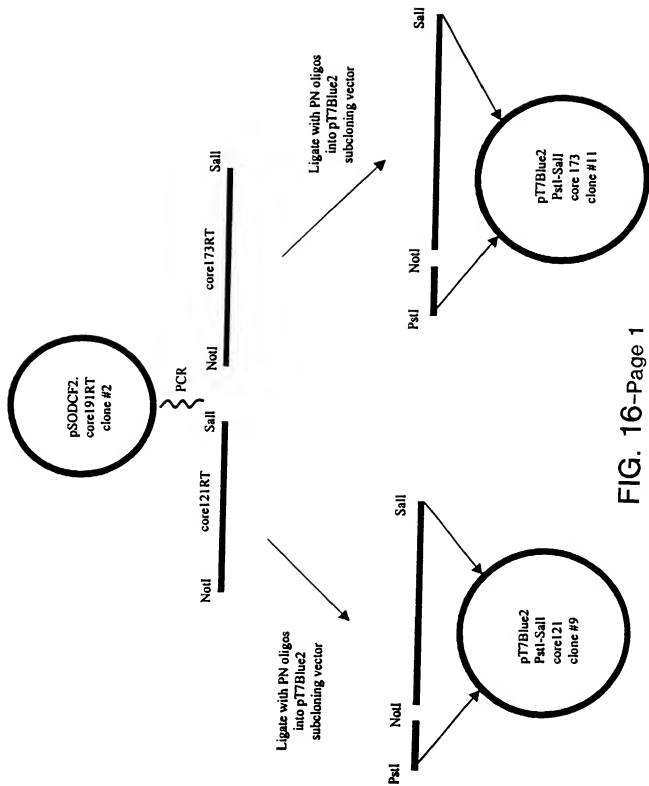


FIG. 16-Page 1

4229 DRD1, 4236 ALWN1,

4262 GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCAAGCCCGCTGGCCATCAAGTCC
 CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTTCAGG
 ^ ^

4301 BGLI, 4308 BALI,

4322 LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
 GAGTGGCTCTCCGAAATACAACCCCGGGAGAAATGGTTAAGTTCCCCCTCTTGACGCCG
 ^

4345 APAI,

4382 TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 TATCGCAGGTGCCGCGCAGCGCGTACTGACAACCTAGCTGTGGTAACACCCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTTGGGGAGTGAACG

4442 TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 TACATCAAGGCCCGGGCAGCCTGTGCGAGCCGAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCGGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCTGACGTGGTACGAGCAC
 ^

4452 SMAI XMAI,

4502 CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 TGTGGCGAGCACTTAGTCGTTATCTGTGAAGCGCGGGGGTCCAGGAGGACGCGGGCAGC
 ACACCGCTGCTGAACCTCAGCAATAGACACTTTCGCGCCCCAGGTCTCTCGCGCGCTCG
 ^ ^

4508 DRD1, 4511 TTH3I,

4562 LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 CTGAGAGCCTTTCACGGAGGCTATGACCAGGTACTCCGCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCTCCGATATGTTCCATGAGCGGGGGGACCCTGGGGGGTGTT

4622 ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTGCACCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGTTGCACAGTCAGCGGGTGCTG
 ^

4637 SACI,

4682 GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
 GGCAGCTGGAAGAGGGTCTACTACCTACCCGTGACCCCTACAACCCCTCGCGAGAGCT
 CCGCGACCTTTCTCCAGATGATGGAGTGGGCGACTGGGATGTTGGGGGAGCGCTCTCGA
 ^

4731 NRUI,

4742 AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
 CGCACCTCTGTGTTCTGTGTGAGGTGAGTTAAGGACCGATCGTTGTATTAGTACAAA

4802 AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
 GCCCCACACTGTGGGGCAGGATGATACTGATGACCCATTCTTTAGCGCTCTTATAGCC
 CGGGGGTGTGACACCCGCTCTACTATGACTACTGGGTAAGAAATCGCAGGAATATCGG
 ^ ^

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

3589 DRA3, 3600 SAC2,

3602 AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
GCGGAAGAACAGAACTGCCCATCAATGCATAAGCAACTCGTTGCTACGTACCACAAAT
CGCCTTCTGTGCTTTGACGGGTAGTTACGTGATTCTGTTAGCAACGATGCAGTGGTGTTA

3611 ALWN1, 3655 PFLM1,

3662 LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTGAC
AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTCCGTCTTCTTCAGTGTAACATG

3681 DRA3,

3722 ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGCGC
TCTGACGTTCAAGACCTGTCGGTAATGGTCTCGATGAGTTCTCTCCAAATTCCTGCGCGCG

3782 SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACAC
AGTTTTCTACTTCCGATTGAACGATAGGCATCTCCTCGAACGTGCGACTGCGGGGTGTG

3816 HIND3,

3842 SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAGACGTCCTGTCATGCCAGAAAGGCC
AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG

3875 AAT2, 3890 BGLI,

3902 ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
GTAACCCACATCAACTCCGTGTGGAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
CATTGGGTGTAGTTGAGGCACACCTTTTGGAAAGACCTTCTGTACATTGGTTATCTG

3962 ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTTCAGCCTGAGAGGGGGTTCGTAAG
TGATGGTAGTACCGATTCTTGCTCCAAAGACGCAAGTCGGACTCTTCCCCCAGCATTC

4022 ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
CCAGCTCGTCTCATCGTGTTCCTCCCGATCTGGGCGTGCCTGTGCGAAAGATGGCTTTG
GGTGAGCAGAGTAGCACAAAGGGGCTAGACCCGACGCGCACACGCTTTTCTACCGAAAC

4082 TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
TACGACGTGGTTACAAAGCTCCCTTGGCCGTGATGGGAAGCTCTACGGATTCCAATAC
ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG

4142 SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
AGTGGTCTGTGCGCCCACTTAAGGAGCACGTTTCGACCTTCAGGTTCTTTTGGGGTTAC

4160 ECORI,

4202 GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
GGGTTCGTATGATACCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
CCCAAGAGCATACTATGGGCGACGAACTGAGGTGTCAGTGACTCTGCTGTAGGCATGC

2942 ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
 ACCGCTAACCATGACTCCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
 TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
 ^ ^
 2966 ESP1, 2969 SAC1,
 3002 GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
 GAGATGGCGCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGAAGTCC
 CTCTACCCGCGGTGTAGTGGTCCCAACTCAGTCTTTTGTTCACCACTAAGACCTGAGG
 3062 PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGAGAAATCCTG
 AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGGCTCTTAGGAC
 ^
 3096 BGL2,
 3122 ArgLysSerArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
 CGGAAGTCTCGGAGATTGCGCCAGGCCCTGCCCGTTTGGGCGCGCGGACTATTAACCCC
 GCCTTCAGAGCCCTCTAAGCGGGTCCGGGACGGGCAACCCGCGGCTGTATTTGGGG
 ^ ^
 3143 ALWN1, 3164 EAG1 XMA3,
 3182 ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
 CCCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACTGTGGTCCATGGCTGCCCG
 GGCATCACCTCTGCACCTTTTCGGGCTGATGCTTGGTGGACACCAAGTACCGACGGC
 ^ ^
 3217 HGIE2, 3229 NCOI,
 3242 LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
 CTTCACCTCCAAAGTCCCTCCTGTGCTCCGCTCGGAAGAGCGGACGGTGGTCCCTC
 GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCTGCCACAGGAG
 3302 ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
 ACTGAATCAACCTATCTACTGCTTGGCCGAGCTCGCCACAGAAGCTTTGGCAGCTCC
 TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAACCGTCGAGG
 ^ ^
 3332 SAC1, 3346 HIND3,
 3362 SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
 TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCTTCTGGC
 AGTTGAAGCGCTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAGACCG
 3422 CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
 TGCCCCCGGACTCCGACGCTGAGTCTATTCTCCTATGCCCCCTGGAGGGGGAGCCT
 ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
 ^
 3437 EAM11051,
 3482 GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
 GGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCCAACCGGAG
 CCCCTAGGCCTAGAATCGCTGCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
 ^ ^ ^
 3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
 3542 AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTACCCCGTGCGCC
 CTACAGCACACGACGAGTTACAGARTGAGAAGCTGTCCGCTGAGCAGTGGGGACGCGG

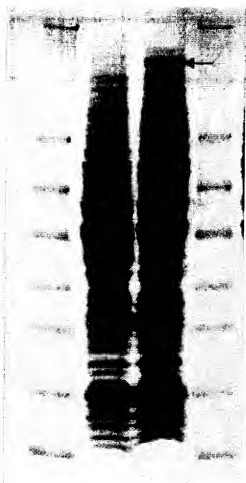


FIG. 15

662 ACGTGTGTCACCCAGACAGTCGATTTACGCCCTTGACCCTACCTTCACCATTGAGACAATC
TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACCTGGGATGGAAGTGTAACCTCTGTTAG

ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys

722 ACGCTCCCCAAGATGCTGCTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
TGCAGAGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCTGACCGTCCCCCTTC

ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer

782 CCAGGCATCTACAGATTTTGTGGCACCGGGGAGCGCCCTCCGGCATGTTTCGACTCGTCC
GGTCCGTAGATGCTAAACACCGTGGCCCCCTCGCGGGAGGCCGTACAAGCTGAGCAGG

816 BGLI, 833 DRD1,

ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr

842 GTCCTCTGTGAGTGTCTATGACGACGGCTGTGCTTGGTATGAGCTACGCCCCGCCGAGACT
ACGGAGACACTCAGGATACTGCGTCCGACACGAACCATCTCGAGTGCGGGCGGCTCTGA

881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu

902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
TGTCATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTCGGTAGAA

931 SMAI XMAI,

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln

962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAAG
CTTAAACCCCTCCCGCAGAAATGTCGGAGTGAGTATATCTACGGGTGAAGATAGGGTCT

985 STUI,

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla

1022 ACAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGGCGCT
TGTTTCGTCTCACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA

1069 DRA3,

ArgAlaGlnAlaProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys

1082 AGGGCTCAAGCCCCCTCCCCATCGTGGGACCATGTGGAAGTGTTTGATTGCGCTCAAG
TCCCGAGTTCGGGGAGGGGTAGCACCTGGTCTACACCTTCACAACTAAGCGGAGTTC

ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle

1142 CCCACCTCCATGGGGCAACACCCCTGCTATACAGACTGGGCGCTGTTGAGAATGAAATC
GGTGGGAGGTACCCGTTGTGGGGACGATATGCTGACCCGCGACAAGTCTTACTTTAG

1150 NCOI,

ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal

1202 ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTGCGCCGACCTGGAGGTC
TGGGACTGCGTGGGTCAGTGGTTTATGTAAGTACTGTACGTACAGCCGGCTGGACCTCCAG

1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu

1262 GTCACAGACACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCTTG
CAGTGCTCTGTGACCCACGACGAACCCCGCAGGACCGACGAAACCGGCGCATACCGGAC

5042 CCCTTGGCAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
 GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
 5064 APAI, 5091 BALI,
 GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
 5102 GGCAGGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAA
 CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTCAGATTT
 5113 NDEI,
 LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
 5162 CTACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
 GAGTGAGGTATTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
 5174 NOTI, 5175 EAGI XMA3, 5182 BALI, 5186 PVU2,
 SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
 5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAAATAGTGTGCGCACAGGTACGGGCCGGGGCGACCTAGACCAAAACG
 5240 DRA3,
 LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP
 5282 CTACTCCTGCTTGTCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGATGAATAGTCGAC
 GTAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGTTGGCTACTTATCAGCTG
 5295 PSTI, 5336 SALI,

FIG. 14-Page 9

4442 TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 TACATCAAGGCCCGGCAGCCTGTCGAGCCGAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGCCGTCGGACAGCTCGGCGTCCCAGGTTCTGACGTGGTACGAGCAC
 ^
 4452 SMAI XMAI,
 CysGlyAspAspLeuValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGACACTTAGTCTGTTATCTGTGAAAGCGCGGGGTCCAGGAGGACGCGCGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCTCTCGCGCCGCTCG
 ^
 4508 DRD1, 4511 TTH3I,
 LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGAGGCTATGACCAGGTACTCCGCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCTCCGATACTGGTCCATGAGGCGGGGGGACCCTGGGGGGTGT
 ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGTCTCTCCAACGTGTGAGTCGCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGTTGCACAGTCAGCGGGTGCTG
 ^
 4637 SACI,
 GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
 4682 GCGCTGGAAAGAGGGTCTACTACCTACCCGTGACCTACAACCCCTCGCGAGAGCT
 CCGCGACCTTCTCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGAGCGCTCTCGA
 ^
 4731 NRUI,
 AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 4742 GCGTGGGAGACAGCAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
 CGCACCTCTGTCTGTTCTGTGTGAGGTGAGTTAAGGACCGATCCGTTGTATTAGTACAAA
 AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
 4802 GCCCCACACTGTGGCGAGGATGATACTGATGACCAATTTCTTAGCGTCTTATAGCC
 CGGGGGTGTGACACCCGCTCTACTATGACTACTGGGTAAGAAATCGCAGGAATATCGG
 ^^
 4806 PFLM1, 4807 DRA3,
 ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu
 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
 TCCCTGGTCGAACCTGTCCGGGAGCTAACGCTCTAGATGCCCGGACGATGAGGTATCTT
 ^
 4893 BGL2,
 ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
 4922 CCCTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
 GGTGACCTAGATGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
 ^
 4954 NCOI,
 SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
 4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACCTGGGGTACCG
 TCAATGAGAGGTCCACTTTAGTTATCCCAACCGGCTACGGAGTCTTTTGAACCCCATGGC
 ^
 5015 SPHI, 5035 KPNI,
 ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly

1884 SACI, 1905 BSPH1,

1922 ProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuVal
CCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCGGAGCCCTCGTA
GGGAGGTGCCTCCTGGACAGTTAGATGACGGGCGGTAGGAGAGCGGCCCTCGGGAGCAT
1934 TTH3I,

1982 ValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaVal
GTCGGCGTGGTCTGTGCAGCAATCTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTG
CAGCCGCACAGACAGCTGTTATGACGCGGCCGTCAACCGGCCGCTCCCCGTCAC
2010 NAEI, 2023 SMAI XMAI,

2042 GlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHis
CAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCAC
GTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAGGGGGTGCCTG
2073 SMAI XMAI, 2099 DRA3,

2102 TyrValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrVal
TACGTGCCGGAGAGCGATGCAGCTGCCCGCTCACTGCCATACTCAGCAGCCTCACTGTA
ATGCACGGCCTCTCGCTACGTCGACGGGCGCAGTACGGGTATGAGTCGTCGGAGTGACAT
2121 PVU2,

2162 ThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSer
ACCCAGCTCCTGAGCGGACTGCACCACTGGATAAGCTCGGAGTGTACCACTCCATGCTCC
TGGGTGAGGACTCCGCTGACGTGGTACCTATTGAGCCCTCACATGGTGGAGGTACGAGG
2165 ALWN1, 2170 MST2,

2222 GlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThr
GGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTAGCGACTTTAAGACC
CCAAGGACCGATTCCCTGTAGACCTGACCTATACGCTCCACAACCTCGTGAAATTTCTGG
2226 ECON1,

2282 TrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArg
TGCTATAAGAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCCTTTGTGTCTGCCAGCGC
ACCGATTTTCGATTTCGATACGGTGTGACGGACCCCTAGGCGAAACACAGGACGGTCGCG
2291 ESI1, 2306 PVU2, 2316 BAMHI,

2342 GlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAla
GGGTATAAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCT
CCCATATTTCCCCAGACCGCTCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGA
2402 GluIleThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArg
GAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGG
CTCTAGTGACCTGTACAGTTTTTGCCTGCTACTCCTAGCAGCAGGATCCTGGAGCTCC
2431 BSAB1, 2447 AVR2, 2454 SSE83871, 2455 PSTI,

2462 AsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeu
AACATGTGGAGTGGGACCTTCCCCATTAATGCCTACACACGGGCCCTGTACCCCCCTT
TTGTACACCTCACCTGGAAGGGGTAATTACGGATGTGGTCCCCGGGACATGGGGGAA

FIG. 11-Page 4

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
 2 AGCTTACAAAACAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
 TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCAGATATTCCACGATCATGAGTTG
 ^
 1 HIND3, 24 NDEI, 52 SCAI,
 ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62 CCCTCTGTGTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAAGGCTCATGGGATCGAT
 GGGAGACAACGACGTTGTGACCCGAAACCAGGAATGTACAGGTTCCGAGTACCCTAGCTA
 ^
 116 CLAI,
 ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCAGTACTCCACC
 GGATTGTAGTCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
 TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 182 TACGGCAAGTTTCCTTGCCGACGGCGGGTGCTCGGGGGGGCGCTTATGACATAAATTTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGGAATACTGTATTATTAACA
 AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
 CTGCTCACGGTGAGGTCCTACGGTGTAGGTAGAACCCTGAACCGTGACAGGAAGTGGTT
 AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 302 GCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
 CGTCTCTGACGCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCCGAGGCAG
 ^
 303 ALWN1,
 ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 362 ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACACCGGAGAGATCCCTTTT
 TGACACGGGGTAGGGTTGTAGTCTCTCCAACGAGACAGGTGGTGCCCTCTTAGGGAAAA
 TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 422 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTGAT
 ATGCCGTTCGATAGGGGGAGCTTCATTAGTTCCCCCTCTGTAGAGTAGAAGACAGTA
 SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 482 TCAAAGAAGAAGTGCGACGAACCTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGGCGTG
 AGTTTCTTCTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
 AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
 542 GCCTACTACCGGGTCTTGACGTGTCCGTATCCCGACCGCGCGATGTTGTGCGTCGTG
 CGGATGATGGCGCCGAACCTGCACAGGCAGTAGGGCTGGTCGCGCTACACAGCAGCAC
 ^
 550 SAC2, 560 DRD1,
 AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
 602 GCAACCGATGCCCTCATGACCGGCTATACCGCGCACTTCGACTCGGTGATAGACTGCAAT
 CGTTGGCTACGGGACTACTGCGCGATATGCGCGCTGAAGCTGAGCCACTATCTGACGTTA
 ^
 615 BSPH1,
 ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle

1322 CysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAla
 TGCTCTCAACAGGCTGCGTGGTCATAGTGGGCAAGGTCTCTTGTCCGGAAGCCGGCA
 ACGGACAGTTGTCCGACGCACCAAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGT
 1375 NAEI,
 1382 IleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGln
 ATCATACCTGACAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGTCTCTCAG
 TAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTC
 1391 DRD1,
 1442 HisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeu
 CACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTC
 GTGAATGGCATGTAGTCTCGTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCGGGAGG
 1502 GlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsn
 GGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCTGTCTGCCAGACCAAC
 CCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTG
 1508 PSTI, 1513 TTH3I,
 1562 TrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGln
 TGGCAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAATTCATCAGTGGGATACAA
 ACCGTTTTTGAAGCTCTGGAAGACCGCTTCGTATACACCTTGAAGTAGTACCCTATGTT
 1571 KHOI, 1592 NDEI,
 1622 TyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhe
 TACTTGGCGGGCTTGTCAACGCTGCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTT
 ATGAACCGCCGAACAGTTGCGACGGACCATTTGGGGCGGTAACGAAGTAACTACCGAAAA
 1649 BSTE2,
 1682 ThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGly
 ACAGCTGCTGTCAACGCGCCACTAACCACTAGCCAAACCCCTCTCTCAACATATTGGGG
 GTGCGACGACAGTGGTGGGGTATTGGTGATCGGTTTGGGAGGAGAAGTTGATTAACCCC
 1683 ALWN1 PVU2,
 1742 GlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGly
 GGGTGGGTGGCTGCCCCAGCTCGCCGCCCGCGTACTGCTTTGTGGCGCTGGC
 CCCACCCACCGACGGGTGAGCGCGGGGCCACGGCGATGACGAAACACCCGCGACCG
 1800 ESp1,
 1802 LeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAla
 TTAGCTGGGCGCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCATAGACATCCTTGCA
 AATCGACCGCGCGGTAGCCGTCAACCTGACCCCTTCAGGAGTATCTGTAGGAACGT
 1808 KASI NARI,
 1862 GlyTyrGlyAlaGlyValAlaGlyAlaValAlaPheLysIleMetSerGlyGluVal
 GGGTATGGCGCGGGCTGGCGGGAGCTCTTGCGGCAATCAAGATCATGAGCGGTGAGGTC
 CCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAAGTTCTAGTACTCGCACTCCAG

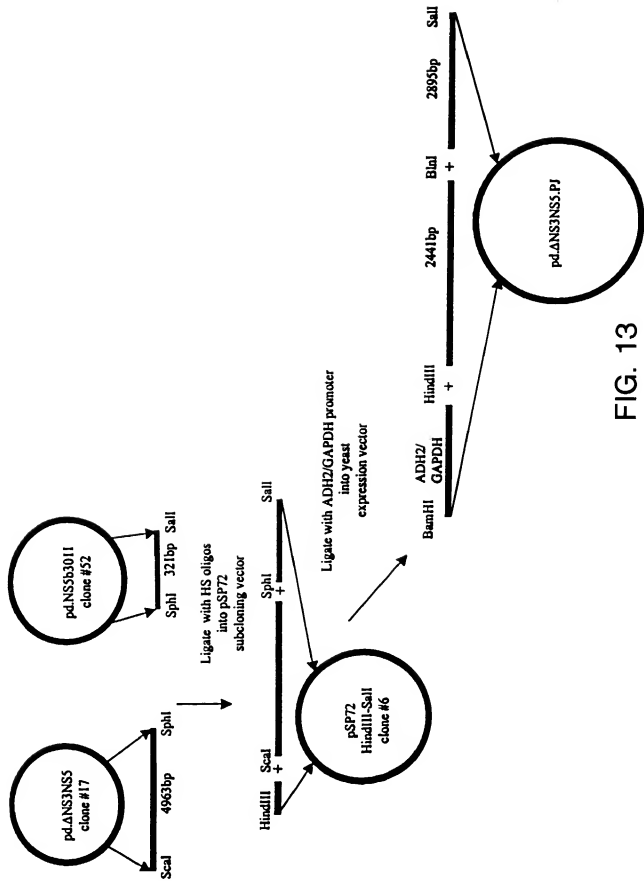


FIG. 13

662 TGCAATACGTGTGTCACCCAGACAGTCGATTTACAGCCTTGACCTTACCTTACCATTTGAG
ACGTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAAGTGGGATGGAAGTGGTAACTC

ThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArg
722 ACAATACAGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTGCGGGCAGGACTGGCAGG
TGTTAGTGGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGCTCGACCGCTC

GlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAsp
782 GGGAGGCCAGGCATCTACAGATTTGTGGCACCCGGGGAGCGCCCTCCGGCATGTTTCGAC
CCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTG
822 BGLI, 839 DRD1,

SerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAla
842 TCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTACGCCCCGCC
AGCAGGCAGGAGACACTCAGGATCTGCGTCCGACAGAACCATACCTGAGTGGCGGGCGG
887 SADI,

GluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAsp
902 GAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGGCCAGGAC
CTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGCACACGGTCTCG
937 SMAI XMAI,

HisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeu
962 CATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCACTTTCTA
GTAGAAGCTTAAACCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGAT
991 STUI,

SerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrVal
1022 TCCGACACAAGCAGAGTGGGGAGAACCTTCTTTACCTGGTAGCGTACCAAGCCACCGTG
AGGGTCTGTTTCGTCTACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGGTGGCAC
1075 DRA3,

CysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArg
1082 TCGCGTAGGGCTCAAGCCCCCTCCCCCATCGTGGGACCATGTGGAAGTGTGTTGATTCCG
ACCGGATCCCGAGTTCGGGGAGGGGGTAGCACCTGGTCTACACCTTCAACAACTAAGCG
1142 LeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsn
CTCAAGCCACACCTCCATGGGCCAACCCCTGCTATACAGACTGGGCGCTGTTGAGAAT
GAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAAGTCTTA
1156 NCOI,

GluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeu
1202 GAAATCACCGTCAGCACCCAGTCACCAATACATCATGATGGATGCGGCCGACCTG
CTTTAGTGGGACTGCGTGGGTGAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGAC
1236 BSPH1, 1240 DRD1, 1243 AVA3, 1251 EAG1 XMA3, 1256 DRD1,

GluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyr
1262 GAGGTCGTACAGGACCTGGGTGCTCGTGTGGCGGGTCTGGCTGCTTTGGCCGCGTAT
CTCCAGCAGTGCTCGTGGACCCAGGACAAACCGCCGAGGACCGACGAAACCGGCGCATA

FIG. 11—Page 2

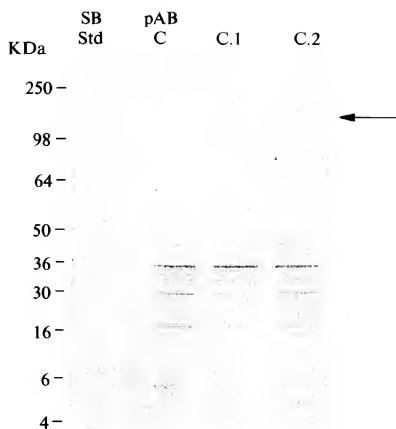


FIG. 12

3782 SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
 TCAAAAGTGAAGGCTAACTTGTCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACAC
 AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTCGAACGTCGGACTGCGGGGGTGTG
 3816 HIND3,
 SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
 3842 TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
 AGTCGGTTTAGGTTCAAACCAATACCCCGTTTCTGCAGGCAACGGTACGGTCTTTCCGG
 3875 AAT2, 3890 BGLI,
 ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
 3902 GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
 CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTACATTGTGGTTATCTG
 ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
 3962 ACTACCATCATGGCTAAGAACGAGGTTTCTGCGTTTCAGCCTGAGAAGGGGGTCTGAAG
 TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTCCCCCAGCATTC
 ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
 4022 CCAGCTCGTCTCATCGTGTTCGCCGATCTGGGCGTGCAGGTCGCGAAAAGATGGCTTTG
 GGTGAGCAGAGTAGCACAAAGGGGCTAGACCCGACGCGCACACGCTTTTCTACCGAAAC
 TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
 4082 TACGACGTGGTTACAAAGCTCCCTTGCCGCTGATGGGAAGCTCCTACGGATTCCAATAC
 ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCTTCGAGGATGCCTAAGGTTATG
 SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
 4142 TCACCAGGACAGCGGGTTGAATTCTCTGCAAGCGTGGAAAGTCCAAGAAAACCCCAATG
 AGTGGTCTCGTCCCAACTTAAGGAGCACGTTTCGACCTTCAGGTCTTTTGGGGTTAC
 4160 ECORI,
 GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
 4202 GGGTCTCTGATGATACCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
 CCCAAGAGCATACTATGGGCGACGAACTGAGGTGTCACTGACTCTCGTGTAGGCATGC
 4229 DRD1, 4236 ALWN1,
 GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
 4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCTGGCCATCAAGTCC
 CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTTCGGGCGACCCGGTAGTTCAGG
 4301 BGLI, 4308 BALI,
 LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
 4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAGTCCGGC
 GAGTGGCTCTCCGAAATACAACCCCGGGAATGGTTAAGTTCCCCCTCTTGAGCCG
 4345 APAI,
 TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 4382 TATCGCAGGTGCCGCGCGAGCGCGTACTGACAACTAGCTGTGGTAACCCCTCACTTGC
 ATAGCGTCCACGCGCGCTCGCCGCATGACTGTTGATCGACACCATTTGTTGGAGTGAACG

FIG. 14-Page 7

GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAAACCCGCGCCGGCCTGATATTGGGG
 3143 ALWN1, 3164 EAG1 XMA3,
 ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
 3182 CCGCTAGTGGAGACGTGGAAAAAGCCGACTACGAACACCTGTGGTCCATGGCTGCCCG
 GCGGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAAGGTACCGACGGGG
 3217 HGIE2, 3229 NCOI,
 LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
 3242 CTTCCACCTCCAAAGTCCCTCCTGTGCCTCGGCCTCGGAAGAAAGCGGACGGTGGTCTC
 GAAGTGGAGGTTTCAGGGGAGGACACGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG
 ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
 3302 ACTGAATCAACCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
 TGACTTAGTTGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCAAACCGTCGAGG
 3332 SACI, 3346 HIND3,
 SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
 3362 TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCTTCTGGC
 AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGAGGAGACTCGGGCGGGGAAGACC
 CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
 3422 TGCCCCCCCCGACTCCGACGCTGAGTCTTCTCCATGCCCCCTGGAGGGGGAGCCT
 ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
 3437 EAM11051,
 GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
 3482 GGGGATCCGGATCTTAGCGACGGGTCTGTTCAACGGTCAGTAGTAGGCGCAACGCGGAG
 CCCCTAGGCCTAGAATCGCTGCCAGTACCAAGTTGCCAGTCATCACTCCGGTTGCGCCTC
 3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
 AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
 3542 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGC
 CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGCGACGCGG
 3589 DRA3, 3600 SAC2,
 AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
 3602 CGGAAGAACAGAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTACCAACAAT
 CGCCTTCTTGCTTTGACGGGTAGTTACGTGATTCTGTAGCAACGATGCAAGTGGTGTTA
 3611 ALWN1, 3655 PFLM1,
 LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
 3662 TTGGTGATTCCACCACTCACGCAGTGCTTGCCAAAGGCAGAAAGTCAATTGAC
 AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGAACCTG
 3681 DRA3,
 ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
 3722 AGACTGCAAGTTCTGGACAGCCATTACCAAGACGTACTCAAGGAGGTAAAGCAGCGCG
 TCTGACGTTCAAGACCTGTGGTAATGGTCTGCATGAGTTCCTCCAATTTCTGTCGCCG

5042 ValProProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAla
 GTACCGCCCTTGGAGCTTGGAGACACCGGGCCGGAGCGTCCGCGCTAGGCTTCTGGCC
 CRTGGCGGGAACGCTCGAACCTCTGTGGCCCGGGCTCGCAGGCGCGATCCGAAGACCGG
 5070 APAI, 5097 BALI,
 ArgGlyGlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLys
 5102 AGAGGAGGCAGGGCTGCCATATGTGGCAAGTACCTTTCAACTGGGCAGTAAGAACAAG
 TCTCCTCCGTCCCGACGGTATACACGGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTC
 5119 NDEI,
 LeuLysLeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAla
 5162 CTCAACTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCT
 GAGTTTGAGTGAGGTTATCGCCGGCGACCGGTGACCTGAACAGGCCGACCAAGTGCCGA
 5180 NOTI, 5181 EAGI XMA3, 5188 BALI, 5192 PVU2,
 GlyTyrSerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrp
 5222 GGCTACAGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCGGCCCGCTGGATCTGG
 CCGATGTGCGCCCTCTGTAAATAGTGTGCGCACAGAGTACGGGCCGGGGCGACCTAGACC
 5246 DRA3,
 PheCysLeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP
 5282 TTTTGCCTACTCTGCTTGTGCGAGGGTAGGCATCTACCTCTCCCCAACCGATGAAGG
 AAAACGGATGAGGACGAACGACGTCCCATCCGTAGATGGAGGAGGGTTGGCTACTTCC
 5301 PSTI, 5331 HGIE2,
 5342 TTGGGGTAAACACTCCGGCCTAAAAAAAAAAAAAAAAATCTAGAACCCGAGTCGAC
 AACCCCATTTGTGAGGCCGGATTTTTTTTTTTTTTTAGATCTTGGGCTCAGCTG
 5378 XBAI, 5390 SALI,

FIG. 11-Page 9

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuVal

2 AGCTTACAAAACAAATTCCACCATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTA
 TCGAATGTTTTTGTAAAGTGGTACCGACGTATACGTCGAGTCCCGATATCCACGATCAT
 ^ ^ ^

1 HIND3, 21 NCOI, 30 NDEI, 58 SCAI,

LeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGly
 62 CTCACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTGCCAAGGCTCATGGG
 GAGTTGGGGAGACAACGACGTTGTGACCCGAAACACGAATGTACAGGTTCCGAGTACCC

IleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyr
 122 ATCGATCCTAACATCAGGACCGGGGTGAGAACATTAACCACTGGCAGCCCCATCAGGTAC
 TAGCTAGGATTGTAGTCTGGGCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATG
 ^

122 CLAI,

SerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIle
 182 TCCACCTACGGCAAGTTCTTGGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATA
 AGGTGGATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGGAATACTGTATTAT

IleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeu
 242 ATTTGTGACGAGTGGCCATCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCCT
 TAAACAGTCTCACGGTGAGGTGCTACGGTGTAGGTAGAACCCTGAACCGTGACAGGAA

AspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGly
 302 GACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGC
 CTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGC
 ^

309 ALWN1,

SerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIle
 362 TCCGTCACGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATC
 AGGCAGTGACACGGGTAGGGTTGTAGTCTCTCCACGAGACAGGTGGTGGCCTCTCTAG

ProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePhe
 422 CCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTC
 GGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCTCTGTAGAGTAGAAG

CysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsn
 482 TGTCTATCAAAGAAGAAGTGCACGAACTCGCCGCAAGCTGGTCGATTGGGCATCAAT
 ACAGTAAGTTTCTTCTTACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTA

AlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValVal
 542 GCCGTGGCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCGAGCGGCGATGTTGTC
 CGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGTACAACAG
 ^ ^

556 SAC2, 566 DRD1,

ValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAsp
 602 GTCTGGCAACCGATGCCCTCATGACCGGCTATACCGCGCACTTCGACTCGGTGATAGAC
 CAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTG
 ^

621 BSPH1,

CysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGlu

FIG. 11-Page 1

Diagram 1

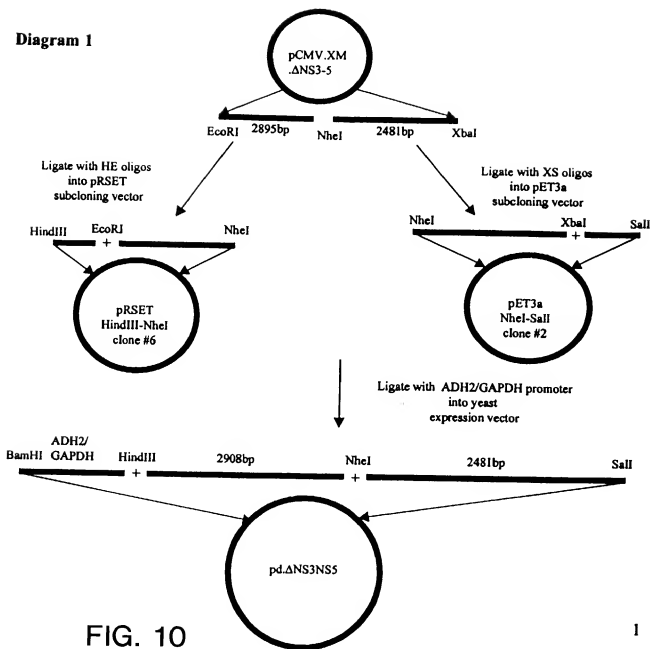


FIG. 10

ACGCCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAG

4442 ThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMet
 ACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCGAGGCTCCAGGACTGCACCATG
 TGAACGATGTAGTTCGGGGCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTAC
 ^

4458 SMAI, XMAI,

4502 LeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAla
 CTCGTGTGTGGCGACGACTTAGTCGTATCTGTGAAAGCGCGGGGTCCAGGAGGACGGG
 GAGCACACCGCTGCTGTAATCAGCAATAGACACTTTCGCGCCCCCAGGTCTCTCTGCGC
 ^ ^

4514 DRD1, 4517 TTH3I,

4562 AlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspPro
 GCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCTGGGGACCC
 CGCTCGGACTCTCGGAAGTGCCTCCGATATGGTCCATGAGGCGGGGGGACCCCTGGGG

4622 ProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAla
 CCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCTGTCGCC
 GGTGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTCACAGTCAGCGG
 ^

4643 SACI,

4682 HisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAla
 CACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCGTGACCCTACAACCCCTCGCG
 GTGCTGCCGCGACCTTCTCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGAGCGC
 ^

4737 NRUI,

4742 ArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIle
 AGAGCTGCGTGGGAGACAGCAAGACACTCCAGTCAATTCTGGCTAGGCAACATAATC
 TCTCGACGCACCCCTCTGTCGTTCTGTGTGAGGTGAGTTAAGGACCGATCCGTTGTATTAG

4802 MetPheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeu
 ATGTTTGGCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTCTTTAGCGTCCTT
 TACAAACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAA
 ^ ^

4812 PFLM1, 4813 DRA3,

4862 IleAlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSer
 ATAGCCAGGGACAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCTGCTACTCC
 TATCGGTCCTGGTCGAACTTGTCGGGAGCTAACGCTCTAGATGCCCGGACGATGAGG
 ^

4899 BGL2,

4922 IleGluProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSer
 ATAGAACCATTGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCA
 TATCTTGGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGGTAAAGT
 ^

4960 NCOI,

4982 LeuHisSerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGly
 CTCACAGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGATGCCTCAGAAAACCTGGG
 GAGGTGTCAATGAGAGGTCCACTTTAGTTATCCCACGGCGTACGGAGTCTTTGAACCC
 ^

5021 SPHI, 5041 KPNI,

3722 TTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCA
 AAACGTCTGACGTTCAAGACCTGTCGGTAATGGTCTGCATGAGTTCCTCCAATTTCGT
 AlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrPro
 3782 GCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGACGCTGACGCC
 CGCCGAGTTTTACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGG
 3822 HIND3,
 ProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArg
 3842 CCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAGACGTCCTTGCCATGCCAGA
 GGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTCTGCAGGCAACGGTATCGGCT
 3881 AAT2, 3896 BGLI,
 LysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrPro
 3902 AAGGCCGTAAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAAATGTAACACCA
 TTCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGT
 IleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGly
 3962 ATAGACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTGAGCTGAGAAAGGGGGT
 TATCTGTGATGGTAGTACCGATTCTTGCTCCAAAGACGCAAGTCGGACTCTTCCCCCA
 ArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMet
 4022 CGTAAGCCAGCTCGTCTCATCGTGTCCCGCATCTGGGCGTGC GCGTGTGCGAAAAGATG
 GCATTTCGTCGAGCAGATAGCACAGGGGCTAGACCCGCACGCGCACACGCTTTTCTAC
 AlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPhe
 4082 GCTTTGTACGAGCTGGTTACAAAGCTCCCTTGGCCGTGATGGGAAGCTCCTACGGATT
 CGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCTTCGAGGATGCCTAAG
 GlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThr
 4142 CAATACTACCAGGACAGCGGGTTGAATTCTCGTGCAAGCGTGGAAGTCCAAGAAAACC
 GTTATGAGTGGTCTGTGCGCCAACTTAAGGAGCAGCTTCGCACCTTCAGTTCCTTTTGG
 4166 ECORI,
 ProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIle
 4202 CCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGCATC
 GGTATCCCCAAGAGCATACTATGGGCGACGAACTGAGGTGTGCTGACTCTCGCTGTAG
 4235 DRD1, 4242 ALWN1,
 ArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIle
 4262 CGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCTGGCCATC
 GCATGCCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCCGGGCGACCGGTAG
 4307 BGLI, 4314 BALI,
 LysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsn
 4322 AAGTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAC
 TTCAGGGAGTGGCTCTCCGAAATACAACCCCGGGAGAATGGTTAAGTTCCCCCTCTTG
 4351 APAI,
 CysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeu
 4382 TGCGGCTATCGCAGGTGCCGCGGAGCGGCTACTGACAACTAGCTGTGGTAACACCCCTC

3122 IleLeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyr
 ATCTCTGCGGAAGTCTCGGAGATTGCCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTAT
 TAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGGCCGGCTGATA
 3149 ALWN1, 3170 EAG1 XMA3,
 AsnProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGly
 3182 AACCCCGCGCTAGTGAGACGTGGAAAAAGCCCGACTACGAACCACTGTGGTCCATGGC
 TTGGGGGGCGATCAGCTCTGCACCTTTTTCGGGCTGATGCTTGGTGACACCAAGTACCG
 3223 HGIE2, 3235 NCOI,
 CysProLeuProProLysSerProProValProProProArgLysLysArgThrVal
 3242 TGCCCGCTTCCACCTCCAAAGTCCCCCTCCTGTGCCTCCGCCCTCGGAAGAAGCGGACGGTG
 ACGGGCGAAGGTGGAGGTTTCAGGGGAGGACACGAGGCGGAGGCTTCTTCGCCTGCCAC
 ValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGly
 3302 GTCCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGC
 CAGGAGTGACTTATTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCG
 3338 SACI, 3352 HIND3,
 SerSerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaPro
 3362 AGCTCTCAACTTCGGGCATTACGGGCGACAATACGACAACATCCTCTAGCGCCGCCCT
 TCGAGGAGTTGAAGGCCGTAATGCCCGCTGTATTGCTGTTGAGGAGACTCGGGCGGGGA
 SerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGly
 3422 TCTGGCTGCCCGGCGACTCCGACGCTGAGTCCTATTCTCCATGCCCGCCCTGGAGGGG
 AGACGCGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCC
 3443 EAM11051,
 GluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsn
 3482 GAGCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAAC
 CTCGGACCCCTAGGCCTAGAATCGCTGCCAGTACCAGTTGCCAGTCATCACTCCGGTTG
 3490 BAMHI, 3491 BSAB1, 3493 BSPE1,
 AlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrPro
 3542 GCGGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCG
 CGCTCTCTACAGCACACGACGAGTTACAGAACTGAGAACCTGTCCGCGTGAGCAGTGGGGC
 3595 DRA3,
 CysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHis
 3602 TGGCGCGGGAAGAAGAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTAC
 ACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCTGTTGAGCAACGATGCAGTG
 3606 SAC2, 3617 ALWN1, 3661 PFLM1,
 HisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThr
 3662 CACAATTTGGTGTATTCCACCACCTCACGCACTGCTTGCCAAAGGCAGAAAGTACACA
 GTGTTAAACACATAAGGTGGTGGAGTGCCTCAGAACGGTTTCCGTCTTCTTCAGTGT
 3687 DRA3,
 PheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAla

pCMV-NS34A

5801	CAAGTCATTC	TGAGAATAGT	GTATGCGGCG	ACCGAGTTGC	TCTTGCCCGG
	GTTCAGTAAG	ACTCTTATCA	CATACGCCGC	TGGCTCAACG	AGAACGGGCC
5851	CGTCAATACG	GGATAATACC	GGCCACATA	GCAGAACTTT	AAAAGTGCTC
	GCAGTTATGC	CCTATTATGG	CGCGGTGTAT	CGTCTTGAAA	TITTCACGAG
5901	ATCATTGGAA	AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT
	TAGTAACCTT	TTGCAAGAAG	CCCCGCTTTT	GAGAGTTCCT	AGAATGGCGA
5951	GTTGAGATCC	AGTTCGATGT	AACCCACTCG	TGCACCCAAC	TGATCTTCAG
	CAACTCTAGG	TCAAGCTACA	TTGGGTGAGC	ACGTGGGTTG	ACTAGAAGTC
6001	CATCTTTTAC	TTTACCAGC	GTTTCTGGGT	GAGCAAAAAC	AGGAAGSCAA
	GTAGAAAATG	AAAGTGGTCG	CAAAGACCCA	CTCGTTTTTG	TCCTCCGTT
6051	AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	GAATACTCAT
	TTACGGCGTT	TTTTCCCTTA	TTCCCGCTGT	GCCTTTACAA	CTTATGAGTA
6101	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA
	TGAGAAGGAA	AAAGTTATAA	TAACCTTCGT	AATAGTCCCA	ATAACAGAGT
6151	TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAARCA	AATAGGGGTT
	ACTCGCCTAT	GTATAAACTT	ACATAAATCT	TTTTATTGTT	TTATCCCCAA
6201	CCGCGCATAT	TTCCCCGAAA	AGTGCCACCT	GACGTCTAAG	AAACCATTAT
	GGCGCGTGTA	AAGGGGCTTT	TCACGGTGGA	CTGCAGATTC	TTTGGTAATA
6251	TATCATGACA	TTAACCTATA	AAAATAGGCG	TATCAGGAGG	CCCTTTCGTC
	ATAGTACTGT	AATTGGATAT	TTTTATCCGC	ATAGTGCTCC	GGGAAGCAG

FIG. 9-Page 8

pCMV-NS34A

4851	AGCAGAGCGA	GGTATGTAGG	CGGTGCTACA	GAGTTCTTGA	AGTGGTGGCC
	TCGTCTCGCT	CCATACATCC	GCCACGATGT	CTCAAGAACT	TCACCAACGG
4901	TAACTACGGC	TACACTAGAA	GGACAGTATT	TGGTATCTGC	GCTCTGCTGA
	ATTGATGCCG	ATGTGATCTT	CCTGTCATAA	ACCATAGACG	CGAGACGACT
4951	AGCCAGTTAC	CTTCGGAAAA	AGAGTTGGTA	GCTCTTGATC	CGGCAAAACAA
	TCGGTCAATG	GAAGCCTTTT	TCTCAACCAT	CGAGAACTAG	GCCGTTTGT
5001	ACCACCGCTG	GTAGCGGTGG	TTTTTTTGT	TGCAAGCAGC	AGATTACGCG
	TGGTGGCGAC	CATCGCCACC	AAAAAAACAA	ACGTTCTGCG	TCTAATGCGC
5051	CAGAAAAAAA	GGATCTCAAG	AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG
	GTCTTTTTTT	CCTAGAGTTC	TTCTAGGAAA	CTAGAAAAGA	TGCCCCAGAC
5101	ACGCTCAGTG	GAACGAAAAA	TCACGTTAAG	GGATTTTGGT	CATGAGATTA
	TGCGAGTCAC	CTTGCTTTTG	AGTGCAATTC	CCTAAAACCA	GTACTCTAAT
5151	TCAAAAAGGA	TCTTCACCTA	GATCCTTTTA	AATTAAAAAT	GAAGTTTTAA
	AGTTTTTTCT	AGAAAGTGGT	CTAGGAAAAA	TTAATTTTTA	CTTCAAAATT
5201	ATCAATCTAA	AGTATATATG	AGTAAACTTG	GTCTGACAGT	TACCAATGCT
	TAGTTAGATT	TCATATATAC	TCATTGGAAC	CAGACTGTCA	ATGGTTACGA
5251	TAATCAGTGA	GGCACCTATC	TCAGCGATCT	GTCTATTTCG	TTCATCCATA
	ATTAGTCACT	CCGTGGATAG	AGTCGCTAGA	CAGATAAAGC	AAGTAGGTAT
5301	GTTGCGTGAC	TCCCGCTCGT	GTAGATAACT	ACGATACGGG	AGGGCTTACC
	CAACGGACTG	AGGGGCAGCA	CATCTATTGA	TGCTATGCCC	TCCCGAATGG
5351	ATCTGGCCCC	AGTGTGCAA	TGATACCGCG	AGACCCACGC	TCACCGGCTC
	TAGACCGGGG	TCACGACGTT	ACTATGGCGC	TCTGGGTGCG	AGTGGCCGAG
5401	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	GAAGGGCCGA	GCGCAGAAAT
	TCGTAAATAG	TCGTTATTTG	GTCGGTCGGC	CTTCCCGGCT	CGCGTCTTCA
5451	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	GTTGCCGGGA
	CCAGGACGTT	GAAATAGGCG	GAGGTAGGTC	AGATAATTAA	CAACGGCCCT
5501	AGCTAGAGTA	AGTAGTTCGC	CAGTTAATAG	TTTGGCGAAC	GTTGTTGCCA
	TCGATCTCAT	TCATCAAGCG	GTCAATTATC	AAACGCGTTG	CAACAACGGT
5551	TTGCTACAGG	CATCGTGGTG	TCACGCTCGT	CGTTTGGTAT	GGCTTCATTC
	AACGATGTCC	GTAGCACCAC	AGTGCGAGCA	GCAAAACATA	CCGAAGTAAG
5601	AGCTCCGGTT	CCCAACGATC	AAGCGAGTT	ACATGATCCC	CCATGTTGTG
	TCGAGGCCAA	GGGTGCTAG	TTCCGCTCAA	TGTACTAGGG	GGTACAACAC
5651	CAAAAAGCG	GTTAGCTCCT	TCGGTCTCC	GATCGTTGTC	AGAAGTAAGT
	GTTTTTTCGC	CAATCAGGGA	AGCCAGGAGG	CTAGCAACAG	TCTTCATTCA
5701	TGGCCGCGT	GTTATCACTC	ATGGTTATGG	CAGCACTGCA	TAATTCCTCT
	ACCGGGGCTA	CAATAGTGAG	TACCAATACC	GTGCTGACGT	ATTAGAGAAA
5751	ACTGTCATGC	CATCCGTAAG	ATGCTTTTCT	GTGACTGGTG	AGTACTCAAC
	TGACAGTACG	GTAGGCATTG	TACGAAAAGA	CAGTGACCAC	TCATGAGTTG

FIG. 9-Page 7

3951 +2 C V V I V G R V V L S G K P A I I
GCGTGGTCAT AGTGGGCAGG GTCGCTCTGT CCGGGAAGCC GGCAATCATA
CGCACCAGTA TCACCCGTCC CAGCAGAACA GGCCCTTCGG CCGTTAGTAT

4001 +2 P D R E V L Y R E F D E M E E C
CCTGACAGGG AAGTCTCTA CCGAGAGTTC GATGAGATGG AAGAGTGCTA
GGACTGTCCC TTCAGGAGAT GGCTCTCAAG CTACTCTACC TTCTCAGAT

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      BamHI      MluI
      ~~~~~
4051 GGATCCCTA   CGCGTTAGAG CTCGCTGATC AGCCTCGACT GTGCCCTTCTA
      CCTAGGTGAT GCGCAATCTC GAGCGACTAG TCGGAGCTGA CACGGAAGAT

```

4101 GTTGCCAGCC ATCTGTTGTT TGCCCCTCCC CCGTGCCTTC CTTGACCCTG
CAACGGTCGG TAGACAACAA ACGGGGAGGG GGCACGGAAG GAACTGGGAC

4151 GAAGGTGCCA CTCCCACTGT CTTTCCTAA TAAAATGAGG AAATTGCATC
CTTCCACGGT GAGGGTGACA GGAAAGGATT ATTTTACTCC TTTAACGTAG

4201 GCATTGTCTG AGTAGGTGTC ATTCTATTCT GGGGGGTGGG GTGGGGCAGG
CGTAACAGAC TCATCCACAG TAAGATAAGA CCCCCACCC CACCCCGTCC

4251 ACAGCAAGGG GGAGGATTGG GAAGACAATA GCAGGCATGC TGGGGAGCTC
TGTCGTTCCC CCTCCTAACC CTTCTGTTAT CGTCCGTACG ACCCCTCGAG

4301 TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC
AAGGCGAAGG AGCGAGTGAC TGAGCGACGC GAGCCAGCAA GCCGACGCCG

4351 GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA
CTCGCCATAG TCGAGTGAGT TTCCGCCATT ATGCCAATAG GTGTCTTAGT

4401 GGGGATAACG CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG
CCCCTATTGC GTCCTTTCTT GTACACTCGT TTTCCGGTCG TTTTCCGGTC

4451 GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG CTCCGCCCCC
CTTGGCATT TCCGGCGCA ACGACCGCAA AAAGGTATCC GAGGCGGGGG

4501 CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
GACTGCTCGT AGTGTTTTTTA GCTGCGAGTT CAGTCTCCAC CGCTTTGGGC

4551 ACAGGACTAT AAAGATACCA GCGGTTTCCC CCTGGAAGCT CCCTCGTGCG
TGTCCTGATA TTTCTATGGT CCGCAAAGGG GGACCTTCGA GGGAGCACGC

4601 CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC
GAGAGGACAA GGCTGGGACG GCGAATGGCC TATGGACAGG CGGAAAGAGG

4651 CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT
GAAGCCCTTC GCACCGCGAA AGAGTTACGA GTGCGACATC CATAGAGTCA

4701 TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCACG AACCCCCCGT
AGCCACATCC AGCAAGCGAG GTTTCACCCG ACACACGTGC TTGGGGGGCA

4751 TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT GAGTCCAACC
AGTCGGGCTG GCGACGCGGA ATAGGCCATT GATAGCAGAA CTCAGGTTGG

4801 CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT
GCCATTCTGT GCTGAATAGC GGTGACCGTC GTCGGTGACC ATTGTCCTAA

2486 ASE1, 2503 APAI,

2522 ProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIle
 CCTGCGCCGAACCTACACGTTTCGCGCTATGGAGGGTGTCTCGAGAGGAATACGTGGGAGATA
 GGACGCGGCTTGATGTGCAAGCGCGATACCTCCACAGACGTCTCCTTATGCACCTCTAT

2559 PSTI,

2582 ArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysPro
 AGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAACTCTTAAATGCCCG
 TCCGTCCACCCCCCTGAAGGTGATGCACCTGCCCATACTGATGACTGTTAGAATTACGGGC

2600 DRA3,

2642 CysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPhe
 TGCCAGGTCCCATCGCCCCGAATTTTTCACAGAATTGGACGGGTGCGCCTACATAGGTTT
 ACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAA

2702 AlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGlu
 GCGCCCCCTGCAAGCCCTTGTGCGGGAGGAGTATCATTAGAGTAGGCTCCAGCAA
 CGCGGGGGGACGTTGCGGAACGACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTT

2762 TyrProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSer
 TACCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCC
 ATGGGCCATCCACGCGTTAATGGAACGCTCGGGCTTGGCTGCACCGGCACAACCTGCAGG

2763 HGIE2, 2815 AAT2,

2822 MetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGly
 ATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGCGAAGGTTGGCGAGGGGA
 TACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGCCCGCTTCCAACCGCTCCCT

2856 EAG1 XMA3,

2882 SerProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAla
 TCACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGTCCATCTCTCAAGGCCA
 AGTGGGGGGAGACACCGGTCGAGGAGCCGATCGGTGATAGCGAGGTAGAGAGTTCCGT

2895 BALI, 2909 NHEI,

2942 ThrCysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrp
 ACTTGCACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGG
 TGAACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACC

2972 ESP1, 2975 SACI,

3002 ArgGlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeu
 AGGCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAGTGGTGATTCTG
 TCCGTCTCTACCCGCGGTTGTAGTGGTCCCACTCAGTCTTTGTTTCACCACTAAGAC

3062 AspSerPheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGlu
 GACTCCTTTCAGTCCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTAACCCGAGAA
 CTGAGGAAGCTAGGCGAACACCGCCTCCTCTGCTCGCCCTCTAGAGGCATGGGCGTCTT

3102 BGL2,

FIG. 11-Page 5

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3251	+2	G D F D S V I D C N T C V T Q T V
		GGCGACTTCG ACTCGGTGAT AGACTGCAAT ACGTGTGTCA CCCAGACAGT CCGCTGAAGC TGAGCCACTA TCTGACGTTA TGCACACAGT GGGTCTGTCA
3301	+2	D F S L D P T F T I E T I T L P
		CGATTTTCAGC CTTGACCCTA CTTTACCACAT TGAGACAATC ACGCTCCCCC GCTAAAGTCG GAAGTGGGAT GGAAGTGGTA ACTCTGTAGT TGCAGGGGGG
3351	+2	Q D A V S R T Q R R G R T G R G K
		AAGATGCTGT CTCCGCACT CAACGTCGGG GCAGGACTGG CAGGGGGGAA TTCTACGAGA GAGGGCGTGA GTTGACGCC CGTCTGACC GTCCCTCTTC
3401	+2	P G I Y R F V A P G E R P S G M F
		CCAGGCATCT ACAGATTGTG GGCACCGGGG GAGCGCCCT CCGGCATGTT GGTCCGTAGA TGTCTAAACA CCGTGGCCCC CTGCGGGGA GGCCTGACAA
3451	+2	D S S V L C E C Y D A G C A W Y
		CGACTCGTCC GTCCTCTGTG AGTGCTATGA CGCAGGCTGT GCTTGGTATG GCTGAGCAGG CAGGAGACAC TCACGATACT GCGTCCGACA CGAACCATAC
3501	+2	E L T P A E T T V R L R A Y M N T
		AGCTCAGGCC CGCCGAGACT ACAGTTAGGC TACGAGCGTA CATGAACACC TCGAGTGCAG GCGGCTCTGA TGTCAATCCG ATGCTCGCAT GTACTTGTGG
3551	+2	P G L P V C Q D H L E F W E G T F
		CCGGGGCTTC CCGTGTGCCA GGACCATCTT GAATTTTGGG AGGGCGTCTT GGCCCCGAAG GGCACACGGT CCTGGTAGAA CTTAAACCC TCCCGCAGAA
3601	+2	T G L T H I D A H F L S Q T K Q
		StuI ----- TACAGGCCTC ACTCATATAG ATGCCCACTT TCTATCCGAG ACAAGCAGA ATGTCCGGAG TGAGTATATC TACGGGTGAA AGATAGGGTC TGTTCGTCT
3651	+2	S G E N L P Y L V A Y Q A T V C A
		GTGGGGAGAA CCTTCCTTAC CTGGTAGCGT ACCAAGCCAC CGTGTGCGCT GACCCCTCTT GGAAGGAATG GACCATCGCA TGGTTCGGTG GCACACCGCA
3701	+2	R A Q A P P P S W D Q M W K C L I
		AGGGCTCAAG CCCCTCCCC ATCGTGGGAC CAGATGTGGA AGTGTGTGAT TCCCGAGTTC GGGGAGGGGG TAGCACCCTG GTCTACACCT TCACAACTA
3751	+2	R L K P T L H G P T P L L Y R L
		TCGCCTCAAG CCCACCTCC ATGGGCCAAC ACCCTGCTA TACAGACTGG AGCGGAGTTC GGGTGGGAGG TACCCGGTTG TGGGGACGAT ATGTCTGACC
3801	+2	G A V Q N E I T L T H P V T K Y I
		GCGCTGTTCA GAATGAAATC ACCCTGACGC ACCCAGTCA CAAATACATC CGGACAAGT CTTACTTTAG TGGGACTGCG TGGGTCAGTG GTTTATGTAG
3851	+2	M T C M S A D L E V V T S T W V L
		ATGACATGCA TGTCCGCCGA CCTGGAGGTC GTCACGAGCA CCTGGGGTCT TACTGTACGT ACAGCCGGCT GGACCTCCAG CAGTGTCTGT GGACCCACGA
3901	+2	V G G V L A A L A A Y C L S T G
		CGTTGGCGGC GTCCTGGCTG CTTTGGCCGC GTATTGCTG TCAACAGGCT GCAACCGCGG CAGGACCGAC GAAACCGGCG CATAACGGAC AGTTGTCCGA

FIG. 9-Page 5

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+2 N S S P P V V P Q S F Q V A H L
2551 TAACCTCCTCT CCACAGTAG TGCCCCAGAG CTTCACGGTG GCTCACCTCC
ATTGAGGAGA GGTGGTCATC ACGGGGTCTC GAAGGTCCAC CGATGGGAGG

+2 H A P T G S G K S T K V P A A Y A
2601 ATGCTCCAC AGGCAGCGGC AAAAGCACCA AGGTCCCGGC TGCATATGCA
TAGCAGGGTG TCCGTCGCGG TTTTCGTGGT TCCAGGGCCG ACGTATACGT

+2 A Q G Y K V L V L N P S V A A T L
2651 GCTCAGGGCT ATAAGGTGCT AGTACTCAAC CCCTCTGTGG CTGCACCACT
CGAGTCCCGA TATTCCACGA TCATGAGTTG GGGAGACAAC GACGTGTGTA

+2 G F G A Y M S K A H G I D P N I
2701 GGGCTTTGGT GCTTACATGT CCAAGGCTCA TGGGATCGAT CCTAACATCA
CCCGAAACCA CGAATGTACA GGTTCGAGT ACCCTAGCTA GGATTGTAGT

+2 R T G V R T I T T G S P I T Y S T
2751 GGACCGGGGT GAGAACAAAT ACCACTGGCA GCCCATCAC GTACTCCACC
CCTGGGCCCCA CTCTTGTTAA TGGTGACCGT CGGGGTAGTG CATGAGGTGG

+2 Y G K F L A D G G C S G G A Y D I
2801 TACGGCAAGT TCCTTGCCGA CGGCGGGTGC TCGGGGGGCG CTTATGACAT
ATGCGGTCA AGGAACGGCT GCCGCCACG AGCCCCCGC GAATACTGTA

+2 I I C D E C H S T D A T S I L G
2851 AATAATTGT GACGAGTGCC ACTCCACGA TGCCACATCC ATCTTGCCGA
TTATTAACA CTGCTCACGG TGAGGTGCCT ACGGTGTAGG TAGAATCCGT

+2 I G T V L D Q A E T A G A R L V V
2901 TTGGCACTGT CCTTGACCAA GCAGAGACTG CGGGGGCGAG ACTGGTTGTG
AACCGTGACA GGAACGTGTT CGTCTCTGAC GCCCCCGCTC TGACCAACAC

+2 L A T A T P P G S V T V P H P N I
2951 CTCGCCACCG CCACCCCTCC GGGCTCCGTC ACTGTGCCCC ATCCCAACAT
GAGCGGTGGC GGTGGGGAGG CCCGAGGCAG TGACACGGGG TAGGGTTGTA

+2 E E V A L S T T G E I P F Y G K
3001 CGAGGAGGTT GCTCTGTCCA CCACCGGAGA GATCCCTTTT TAGCGCAAGG
GCTCCTCCAA CGAGACAGGT GGTGGCCTCT CTAGGGAAAA ATGCCGTTC

+2 A I P L E V I K G G R H L I F C H
3051 CTATCCCCCT CGAAGTAATC AAGGGGGGGA GACATCTCAT CTTCGTGCAT
GATAGGGGGA GCTTCATTAG TTCCCCCCT CTGTAGAGTA GAAGACAGTA

+2 S K K K C D E L A A K L V A L G I
3101 TCAAAGAAGA AGTGCGACGA ACTCGCCGCA AAGCTGGTCG CATTGGGCAT
AGTTTCTTCT TCACGCTGCT TGAGCGGCGT TTCGACCAGC GTAACCCGTA

+2 N A V A Y Y R G L D V S V I P T
3151 CAAATGCCGT GCCTACTACC GCGGTCTTGA CGTGTCCGTC ATCCCGACCA
GTTACGGCAC CGGATGATGG GCACAGAACT GCACAGGCAG TAGGGCTGGT

+2 S G D V V V V A T D A L M T G Y T
3201 GCGGCGATGT TGTGTCGTG GCAACCGATG CCCTCATGAC CGGCTATACC
CGCCGCTACA ACAGCAGCAC CGTTGGCTAC GGGAGTACTG GCCGATATGG

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1851	TTAACGGTGG	AGGGCAGTGT	AGTCTGAGCA	GTACTCGTTG	CTGCCGCGCG	AATTGCCACC	TCCCGTCACA	TCAGACTCGT	CATGAGCAAC	GACGCGCGCG						
1901	CGCCACCAGA	CATAATAGCT	GACAGACTAA	CAGACTGTTC	CTTTCCATGG	GCGGTGGTCT	GTATTATCGA	CTGTCTGATT	GTCTGACAA	GAAAGGTACC						
+2	EcoRI ----- M A P															
1951	GTCTTTTCTG	CAGTCACCGT	CGTCGACCTA	AGAATTACCC	ATGGCGCCCA	CAGAAAAGAC	GTCAGTGGCA	GCAGCTGGAT	TCTTAAGTGG	TACCGCGGGT						
+2	I T A Y	A Q Q	T R G L	L G C	I I T	TCACGGCGTA	CGCCCAGCAG	ACAAGGGGCC	TCCTAGGGTG	CATAATCACC	AGTGCCGCAT	GCGGGTCGTC	TGTTCCCGCG	AGGATCCCA	GTATTAGTGG	
2051	+2	S L T G	R D K	N Q V	E G E V	Q I V	AGCCTAACTG	GCCGGGACAA	AAACCAAGTG	GAGGGTGAGG	TCCAGATTGT	TCGGATTGAC	GCGCCCTGTT	TTTGTTTCAC	CTCCCACCTC	AGGTCTAACAA
2101	+2	S T A	A Q T F	L A T	C I N	G V C	GTCAACTGCT	GCCCAAACCT	TCCTGGCAAC	GTGCATCAAT	GGGGTGTGCT	CAGTTGACGA	GCGGTTTGGG	AGGACCGTTG	CACGTAGTTA	CCCCACACGA
2151	+2	W T V Y	H G A	G T R T	I A S	P K G	GGACTGTCTA	CCACGGGGCC	GGAACGAGGA	CCATCGCGTC	ACCCAAGGGT	CCTGACAGAT	GGTGCCCGG	CCTTGCTCCT	GGTAGCGCAG	TGGGTTCCCA
2201	-2	P V I Q	M Y T	N V D	Q D L V	G W P	CCTGTCTATCC	AGATGTATAC	CAATGTAGAC	CAAGACCTTG	TGGGCTGGCC	GGACAGTAGG	TCTACATATG	GTTACATCTG	GTCTGGAAC	ACCCGACCCG
2251	+2	A S Q	G T R S	L T P	C T C	G S S	CGCTTCGCAA	GGTACCCGCT	CATTGACACC	CTGCACCTTG	GGCTCCTCGG	GCGAAGCGTT	CCATGGGCGA	GTAAGTGTGG	GACGTGAACG	CCGAGGAGCC
2301	+2	D L Y L	V T R	H A D V	I P V	R R R	ACCTTTACCT	GGTCACGAGG	CACGCCGATG	TCATTCCCGT	GCGCCGGCGG	TGGAAATGGA	CCAGTGCTCC	GTGCGGCTAC	AGTAAGGGCA	GCGGGCGCCG
2351	+2	G D S R	G S L	L S P	R P I S	Y L K	GGTGATAGCA	GGGGCAGCCT	GCTGTGCCCC	CGGCCCATTT	CCTACTTGAA	CCACTA7CGT	CCCCGTCCGA	CGACAGCGGG	GCCGGGTAAA	GGATGAACCT
2401	+2	G S S	G G P L	L C P	A G H A	V G	AGGCTCCTCG	GGGGGTCCCG	TGTTGTGCCC	CGCGGGGCAC	GCCGTGGGCA	TCCGAGGAGC	CCCCACGGCG	ACAACACGGG	GCGCCCCGTG	CGGCACCCGT
2451	+2	I F R A	A V C	T R G V	A K A	V D F	TATTAGGGC	GCGGTGTGTC	ACCCGTGGAG	TGGCTAAGGC	GVTGGACTTT	ATAAATCCCG	GCGCCACACG	TGGGCACCTC	ACCGATTCCG	CCACTCTGAAA
2501	+2	I P V E	N L E	T T M	R S P V	F T D	ATCCCTGTGG	AGAACCTAGA	GACAACCATG	AGGTCCCCGG	TGTTACGGGA	TAGGGACACC	TCTTGATCT	CTGTTGGTAC	TCCAGGGGCC	ACAAGTGCCCT

FIG. 9-Page 3

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901	TTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ATAACCCCGC AAAAACCGTG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TATTGGGGCG
951	CCCGTTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GGGCAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT
1001	GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC CGTCTCGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC CTATGGTGGC
1051	TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGGGGCGC ACAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCCCGCGC
1101	GGAACGGTGC ATTGGAACGC GGATTCCCGC TGCCAAGAGT GACGTAAGTA CCTTGCCACG TAACCTTGCG CTAAGGGGCG ACGGTTCCTCA CTGCATTCTAT
1151	CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA GGCGGATATC TGAGATATCC GTGTGGGGAA ACCGAGAATA CGTACGATAT
1201	CTGTTTTTGG CTGGGGGCT ATACACCCCC GCTCCTTATG CTATAGGTGA GACAAAAACC GAACCCCGGA TATGTGGGGG CGAGGAATAC GATATCCACT
1251	TGGTATAGCT TAGCCTATAG GTGTGGGTGA TTGACCATTA TTGACCACT ACCATATCGA ATCGGATATC CACACCCAAT AACTGGTAAT AACTGGTGAG
1301	CCCTATTGGT GACGATACTT TCCATTACTA ATCCATAACA TGGCTCTTTG GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC
1351	CCACAACAT CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT GGTGTGATA GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTGA
1401	GACACGGACT CTGTATTTTT ACAGGATGGG GTCCATTAT TATTACAACA CTGTGCCTGA GACATAAAAA TGTCTACCC CAGGTAAATA ATAAATGTTT
1451	TTACATATA CAACAACGCC GTCCCCCGTG CCGCGAGTTT TTATTAACA AAGTGATAT GTTGTTCGGC CAGGGGGCAC GGGCGTCAAA AATAATTTGT
1501	TAGCGTGGA TCTCCGACAT CTCGGGTACG TGTTCGGAC ATGGGCTCTT ATCGCACCT AGAGGCTGTA GAGCCATGC ACAAAGCCTG TACCCGAGAA
1551	CTCCGGTAGC GGCAGGACTT CCACATCCGA GCCCTGGTCC CATCCGTCCA GAGGCCATCG CCGCCTCGAA GGTGTAGGCT CGGGACACAG GTAGCGAGGT
1601	GCGGCTCATG GTCGCTCGGC AGCTCCTTGC TCCTAACAGT GGAGGCCAGA CGCCGAGTAC CAGCGAGCCG TCGAGGAACG AGGATTGTCA CCTCCGGTCT
1651	CTTAGGCACA GCACAATGCC CACCACCACC AGTGTGCCGC ACAAGGCCGT GAATCCGTGT CGTGTACCG GTGGTGGTGG TCACACGGCG TGTTCGGCA
1701	GGCGGTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGCACCT CCGCCATCCC ATACACAGAC TTTTACTCGA GCCTCTAACC CGAGCGTGGA
1751	GGACGCAGAT GGAAGACTTA AGGCAGCGGC AGAAGAAGAT GCAGGCAGCT CCTGCGTCTA CCTTCTGAAT TCCGTGCCCG TCTTCTCTA CGTCCGTGCA
1801	GAGTTGTTGT ATTCTGATAA GAGTCAGAGG TAACTCCCGT TGCGGTGCTG CTCAACAACA TAAGACTATT CTCAGTCTCC ATTGAGGGCA ACGCCACGAC

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1	TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG
	AGCGCGCAAA	GCCACTACTG	CCACTTTTGG	AGACTGTGTA	CGTCGAGGGC
51	GAGACGGTCA	CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG
	CTCTGCCAGT	GTCGAACAGA	CATTGCGCTA	CGGCCCTCGT	CTGTTCGGGG
101	TCAGGGCGCG	TCAGCGGGTG	TTGGCGGGTG	TCGGGGCTGG	CTTAACATAG
	AGTCCCGCGC	AGTCGCCAC	AACCGCCAC	AGCCCCGACC	GAATTGATAC
151	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	ACCATATGAA	GCTTTTGTGA
	GCCGTAGTCT	CGTCTAACAT	GACTCTCACG	TGGTATACTT	CGAAAAACGT
<p style="text-align: center;">StuI -----</p>					
201	AAAGCCTAGG	CCTCCAAAAA	AGCCTCCTCA	CTACTTCTGG	AATAGCTCAG
	TTTCGGATCC	GGAGGTTTTT	TCGGAGGAGT	GATGAAGACC	TTATCGAGTC
251	AGGCCGAGGC	GGCCTCGGCC	TCTGCATAAA	TAAAAAAAT	TAGTCAGCCA
	TCGGGCTCCG	CCGGAGCCGG	AGACGTATTT	ATTTTTTTTA	ATCAGTCGGT
301	TGGGGCGGAG	AATGGGCGGA	ACTGGGCGGG	GAGGGAATTA	TTGGCTATTG
	ACCCGCGCTC	TTACCCGCCT	TGACCCGCCC	CTCCCTTAAT	AACCGATAAC
351	GCCATTGCAT	ACGTTGTATC	TATATCATAA	TATGTACATT	TATATTGGCT
	CGGTAACGTA	TGCAACATAG	ATATAGTATT	ATACATGTAA	ATATAACCGA
401	CATGTCCAAT	ATGACCGCCA	TGTTGACATT	GATTATTGAC	TAGTTATTAA
	GTACAGGTTA	TACTGGCGGT	ACAACGTAA	CTAATAACTG	ATCAATAATT
451	TAGTAATCAA	TTACGGGGTC	ATTAGTTCAT	AGCCCATATA	TGGAGTTCGG
	ATCATTAGTT	AATGCCCCAG	TAATCAAGTA	TCGGGTATAT	ACCTCAAGGC
501	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG	CCCAACGACC
	GCAATGTATT	GAATGCCATT	TACGGGGCGG	ACCGACTGGC	GGGTTGCTGG
551	CCCGCCCAT	GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA
	GGGCGGGTAA	CTGCAGTTAT	TACTGCATAC	AAGGGTATCA	TTGCGGTTAT
601	GGGACTTTCC	ATTGACGTCA	ATGGGTGGAG	TATTTACGGT	AAACTGCCCA
	CCCTGAAAGG	TAACCTGCAGT	TACCCACCTC	ATAAATGCCA	TTTGACGGGT
651	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC	AAGTCCGCCC	CCTATTGACG
	GAACCGTCAT	GTAGTTCACA	TAGTATACGG	TTCAGGCGGG	GGATAACTGC
701	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCAGGTA	CATGACCTTA
	AGTTACTGCC	ATTACCGGG	CGGACCGTAA	TACGGGTGAT	GTAATGGAAT
751	CGGGACTTTC	CTACTTGCCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC
	GCCTGAAAG	GATGAACCGT	CATGTAGATG	CATAATCAGT	ACGGATAATG
801	CATGGTGATG	CGGTTTGGC	AGTACACCAA	TGGGCGTGGA	TAGCGGTTTG
	GTACCACTAC	GCCAAAACCG	TCATGTGGTT	ACCCGCACCT	ATCGCCAAAC
851	ACTCACGGGG	ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG
	TGAGTGCCCC	TAAAGGTTCA	GAGGTGGGGT	AACTGCAGTT	ACCTCAAAAC

FIG. 9-Page 1

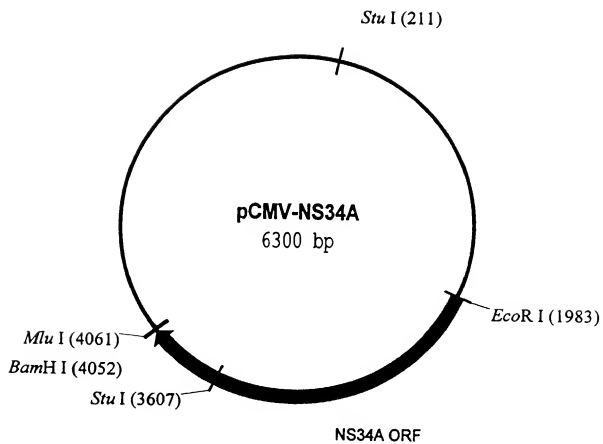


FIG. 8

pCMV-II

3521	TTGCCATTGC TACAGGCATC GTGGTGTAC GCTCGTCTGT TGGTATGGCT TCATTACGCT CGGGTTCCCA ACCATCAAGG AACGGTAACG ATGTCGGTAG CACCACAGTG CGAGCAGCAA ACCATACCGA AGTAAGTCGA GCGCAAGGGT TCGTAGTTCC
3601	CGAGTTAGAT GATCGCCCAT GTTCTCAAA AAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTGAGAA GTAAGTTGGC GCTCAATCTA CTAGGGGTA CACACGTTT TTTCGCCAAT CGAGGAAGCC AGGAGGTAG CAACAGTCTT CATTTCAACCG
3681	CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT TCCTTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CGCTCAAT ACTGAGTACC AATACGGTGG TCACCTATTA AGAAGATGAC AGTACGGTAG GCAITTTACG AAAAGACACT
3761	CTGCTGAGTA CTCACCCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGTCTTT GCCGGCGTC AATACGGGAT GACCACCTCAT GAGTTGGTTC AGTAAGACTC TTATCACATA CCGCGCTGCG TCAACGAGAA CGGGCCGCG TTAGCGCCTA
3841	AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAAAG TTCTTCGGGG CGAAAACTCT CAAGGATCTT TTATGGCGCG GTGTATCGTC TTCAAAATTT CACGAGTAGI AACCTTTTGC AAGAAGCCCC GCTTTTGAGA GTTCTTAGAA
3921	ACCGCTGTTG AGATCCAGTT CGATGTAACC CACTCGTGCA CGCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTTT TGGCGACAAC TCTAGGTCAA GCTACATTGG GTGAGCACGT GGGTTGACTA GAAGTCGTAG AAAATGAAG TGGTCGCAAA
4001	CTGGGTGAGC AAAAACAGGA AGCCAAAATG CCGCAAAAAA GGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC GACCCACTCG TTTTGTCTT TCGGTTTAC GGGGTTTTT CCCTTATTC CGCTGTGCT TTACAACCTA TGAATATGAG
4081	TTCTTTTTTC AATATTATTG AAGCATTAT CAGGGTTATT GTCTCATCAG CGGATACATA TTGAATGTA TTAGAAAAA AAGGAAAAAG TTATAATAAC TTGCTAAATA GTCCCAATAA CAGAGTACTC GCTATGTAT AAATTTACAT AAATCTTTT
4161	TAAACAAATA GGGGTTCCGC GGACATTTCC CGAAAAAGT CCAGCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA ATTGTGTTAT CCCCAGGGG CGTGTAAGG GGTGTTTTC AGATTCTTG GTAATAATAG TACTGTAAIT
4241	CTTATAAAAA TAGCGGTATC AGGAGGCCCT TTCGTC GGATATTTT ATCCGATAG TGTCCCGGA AAGCAG

FIG. 7 -Page 6

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2801	TCGCAGCAGC CACTGTAAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG GTGCGCTAAC ACCGTCGTCG GTGACCAATG TCCTAATCGT CTCGCTCCAT ACATCGGCCA CGATCTCTCA AGAACTTAC CACCGGATTG
2881	TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTGGCGTC TGCTGAAGCG AGTTACCTTC GGAAAAAGAG TTGTAGCTAG ATGCGGATGT GATCTTCCGT TCATAACCA TAGACGGGAG ACCACTGGG TCAATGGAAG CCTTTTCTC AACCATCGAG
2961	TTGATCCGGC AACAAACCA CCGCTGGTAG CGGTGTTT TTGTTTGA AGCAGCAGAT TACGCGCAGA AAAAAAGCAT AACTAGCGCG TTGTATTGT GGCACCATC GGCACCAAAA AAACAAACCT TCGTCGCTA ATGCGCGTCT TTTTTCCTA
3041	CTCAAGAAGA TCGTTTGATC TTTTCTACGG GGTCTGAGCG TCAGTCGGAAC GAAAACTCAC GTTAAAGGAT TTTGGTCATG GAGTTCTTCT AGGAACTAG AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTGAAGTG CAATTCCCTA AAACCACTAC
3121	AGATTATCAA AAAGGATCTT CACTAGATC CTTTAAAT AAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA TCTAATAGTT TTTCTAGAA GTGGATCTAG GAAATTTAA TTTTACTTC AAAATTTAGT TAGATTTTAT ATATACTCAT
3201	AACTTGTCTT GACAGTTACC AATGCTTAAT CAGTCAGGCA CCTATCTCAG CGATCTGTCT ATTTGTTTCA TCCATAGTTG TTGAACCGA CTGTCAATGG TTAGCAATTA CTCACTCCGT GGATAGAGTC GCTAGACAGA TAAACCAAGT AGGTATCAAC
3281	CCTGACTCCC CGTCTGTAG ATAACTACGA TACGGGAGGG CTTACCATCT GGGCCCAAGT CTGCAATCAT ACGCGAGAC GGACTGAGGG GCAGCACATC TATTGATGCT ATGCCCTCCC GAATGGTAGA CCGGGGTCTAC GACGTTACTA TGGCGTCTG
3361	CCAGGCTCAC CGGCTCCAGA TTTATCAGA ATAAACGAGC CAGCGGGAAG GCGGAGCGCG AGAAGTGGT CTGCAACTTT GGTGGGAGTG GCGGAGTCT AAATAGTCT TATTGGTGG CTCGGGCTTC CCGGCTCGCG TCTTACCAG GACGTTGAAA
3441	ATCGGCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TAGGCGGAGG TAGGTCAGAT AATTAAACAC GGCCCTTCCA TCTCATTCAT CAAGCGGTCA ATTATCAAC GGGTTCCAAC

FIG. 7 - Page 5

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2081	CCAGGCATCT GTTGTGGC GCTCCCGCT GCTTCCCTTG ACCCTGAAG GTGCCACTCC CACTGTCCCT TCCTAATAAA GCTCGGTAGA CAACAACGG GGAGGGGGCA CGGAGGAAC TGGGACCTTC CACGGTGAGG GTGACAGGAA AGGATTATTT
2161	ATGAGGAAT TGCATCGCAT TGTCTGAGTA GGTGTCAITC TATTCTGGG GGTGGGTGG GGCAGGACAG CAAGGGGAG TACTCCITTA ACGTAGCGTA ACAGACTCAT CCACAGTAAG ATAAGACCCC GCACCCACC CCGTCTCTGC GTTCCCTC
2241	GATTGGGAG ACAATAGCAG CCATCTGCGG GAGCTCTTCC GCTTCCTGG TCACTGACT GGTGCGCTCG GTCTTCCGG CTAACCCCTC TGTATCGTC GTTACGACCC CTCGAGAAG CGAAGGAGCG AGTCACTGAG CGACGGGAGC CAGCAAGCCG
2321	TCCGGCGAGC GGTATCAGCT CACTCAAAG CGGTAATAC GTTATCCACA GAATCAGGG ATAAACCAGG AAAGAATG ACGCCGCTCG CCATAGTGA GTGAGTTTC GGCATTATGC CAATAGGTGT CTTAGTCCCC TATTGGTCC TTCTTGTAC
2401	TCAGCAAAAG GCGAGCAAA GGCAGGAAC CGTAAAAAG CCGCTTGTCT GCGTCTTTC CATAGCTCC GCGCCCTGA ACTCGTTTC CGGTGCTTT CCGTCTCTG GCAATTTTCC GCGCAACGA CCGCAAAAAG GTATCCGAG CGGGGGGACT
2481	CGAGCATCAC AAAATCGAC GCTCAAGTCA GAGTGGCGA AAGCCGACAG GACTATAAG ATACAGGCG TTTCCCGCTG GCTCGTAGT TTTTAGCTG CGAGTCAGT CTCACCGCT ITGGGTGTG CTGATTTTC TATGTCTCCG AAAAGGGGAC
2561	GAAGTCCCT CGTGGCTCT CCTGTTCCGA CCGTCCGCT TAGCGGATAC CTGTCCGCT TTCTCCCTTC GGAAGCGCTG CTTCGAGGA GCACGCGA GAACAAGCT GGGAGCGGA ATGGCTATG GACAGCGGA AAGAGGAAG CCCTTCGCAC
2641	CGCGTTTCTC AATGCTCAG CTGTAGGTAT CTCAGTTCCG TGTAGTCTG TCGTCCAG CTGGGCTGTG TGCACGAAC CGGAAAGG TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGA AGCGAGTTC GACCCGACAC ACCTGTCTGG
2721	CCCGGTTTCA GCGGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT CCAACCCGCT AAGACAGAC TTATCGCCAC GGGCAAGTC GGGCTGGGA CGCGGAATAG CCCATTGATA GCAGAACTCA GGTGGGCA TTCTGTGCTG AATAGGGTGT

FIG. 7-Page 4

pCMV-11

1441	TATTACAAA TTACATATA CAACAACGCC GTCCCGCCGTC CCCGACGTTT TTATTAACA TAGCTGGGA TCTCGACAT ATAAATGTTT AAGTGATAT GTTGTGGG CAGGGGCAC GGGGCTAAA AATAATTTT ATCGACCCCT ACAGGCTGTA
1521	CTCGGTAGG TGTTCGGGAC ATGGGCTCTT CTCGGTAGC GCGGAGCTT CCACATCGGA GCGTGTAGCT CCGGACCAGG GTAGCAGGT GAGCCCATGC ACAAGGCTG TACCGGAAA GAGGCGATCG CCGGCTGAA GGTGTAGCT CCGGACCAGG GTAGCAGGT
1601	GGGGCTCATG GTGGCTCGG ACCTCCTTGC TCCTAACAGT GGAGGCCAGA CTTAGGCCA GCACAATGCC CACCACCACG GCCCCAGTAC CAGCGAGCGG TCGAGGAACG AGAATTGCA CTCGCGTCT GAATCCGTCT CGTGTTACGG GTGGTGGTGG
1681	ACTGTGCGG ACAAGGCCGT GCGGTAGGG TATGTCTTG AAAATGAGCT CGGAGATTGG GCTCGCACTT GGAGCCAGAT TCACACGGCG TGTTCGGGCA CCGCATCC ATACACAGC TTTTACTCGA GCTCTAAC CGAGCGTGGA CTTGCGTCTA
1761	GGAAGACTTA AGCAGCGCG AGAAGAGAT GCAGGCAGCT GAGTGTGTTG ATTTGATAA GAGTCAAGG TAACGCCCT CCTTCTGAT TCGTGCGCG TCTTCTTCTA CTTGCTGCGA CTCAACAACA TAAGACTATT CTCAGTCTCC ATTGAGGCGA
1841	TGCGGTGCTG TTAAGGTGG AGGCAGTGT ACTCTGACA GTACTCGTTG CTGCGCGGCG CGGCCACCAGA CATAATAGCT ACGCCACGAC AATTGCCACC TCCGCTACA TCAGACTCGT CATGAGCAAC GACGGCGCG GCGGTGCTCT GTATTATCGA
1921	GACAGACTAA CAGACTGTTG CTTTCCATGG CTCCTTTCTG CAGTACCGCT CGTCGACCTA AGAATTCAGA CTGAGGCAAG CTGTCTGATT GTCTCACAG GAAGGTACC CAGAAAGAC GTACGTGGGA GCAGCTGGAT TCTTAAGTCT GAGCTCGTTC
	XbaI BamHI MluI
2001	TCTAGAAAG CGCGCAAGA TATCAAGAT CCACTACGCG TTAGAGTCCG CTGATCAGCC TCGACTGTGC CTTCTAGTTG AGATCTTTC GGGGGTTCT ATAGTCTCTA GGTGATCGG AATCTGAGC GACTAGTCG ACCTGACAGC GAAGATCAAC

EcoRI

FIG. 7 -Page 3

pCMV-II

721	GCCTGGCAATT ATGCCCAAGTA CATGACCTTA CGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGTATTATC CGGACCGGTAA TACGGGTCTAT TACTTGAAT GCCTGAAAG GATGAACCGT CATGTAGATG CATAATCACT ACCGATAATG
801	CATGCTGATG CGGTTTGGC AGTACACCAA TGGGGCTGGA TAGGGTTTG ACTCACGGG ATTTCACACT CTCACACCCA GTACCACTAC GCCAAACCG TCATGTGTTT ACCCGCACT ATCCCAAC TCAGTGCACC TAAAGTTCA GAGTGGGGT
881	TTGACGTCAA TGGGAGTTTG TTTTGGCACC AAAATCAAGG GGAATTTCCT AAAATCTGTA ATAAACCCGC CCCCTTGACG AACTGCACTT ACCTCAAAAC AAAACCGTGG TTTTACTTGC CCTGAAAGT TTTACAGCAT TATTGGGGGG GGGCAACTGC
961	CAAATGGCGG GTAGGCTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTACTGAA CCGTCAGATCG CCTGGAGACG GTTTACCCGC CATCCGGACA TGCCACCTC CAGATATATT CGTCTGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC
1041	CCATCCACGC TGTTTTGACC TCCATAGAAG ACACGGGAC CGATCCAGCC TCCGGGGCGG GGAACGCTGC ATTGGAACGC GGTAGGTGCG ACAAACCTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCCGCG CCTTGGCCAGC TAACTTTGG
1121	GGATTCCCGG TGCCAAGACT GACGTAAAGTA CGGCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA CCTAAGGGGC ACGGTTCTCA CTGCAATTCTAT GCGGATATC TGAGATATCC GTGTGGGAA ACCGAGAATA CGTACGATAT
1201	CTGTTTTTGG CTTGGGGCCT ATACACCCGC GCTCCTTATG CTATAGTGA TGCTATAGCT TAGCCTATAG GTGTGGGTGA GACAAAAACC GAACCCGGGA TAATGGGGG CGAGGAATAC GATATCCACT ACCATATCGA ATCGGATATC CACACCAAT
1281	TTGACCAATTA TTGACCACTC CCCTATTGGT GACGATACCT TCCATTACTA ATCCATAACA TGGCTCTTTG CCACAACATAT AACTGGTAAT AACTGGGTGAG GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC GGTCTTGATA
1361	CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT GACACGGACT CTGTATTTTT ACAGGATGGG GTCCATTAT GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTGA CTGTGCTGTA GACATAAAAA TGTCTTACCC CAGTAATAA

FIG. 7 -Page 2

pCMV-II

1	TCGGCGCTTT CGGTGATGAC GGTCAAAACC TCTGACACAT GCAGCTCCCG CAGACGGTCA CAGCTTGTCT GTAAGGGGAT AGCGCGGAAA GGCATCTAGT CCACCTTTGG AGACTGTGTA CGTCGAGGGC CTCTGCCAGT GTCGAACAGA CATTCGCTTA
81	CGCGGGAGCA GACAAAGCCG TCAGGGGGG TCAGCGGGT TTGGCGGGTG TCGGGGGCTG CTTAACTATG CGGCATCAGA CGGCCCTCGT CTGTTCGGGC AGTCGGCGC AGTCGCCAC AAGCGGCCAC AGCCCCGACC GAATTCATAC GCGGTACTCT
161	GCAGATTGTA CTGAGAGTGC ACCATATGAA GCTTTTTCGA AAGCCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG GGCTAAACAT GACTCTCAG TGGTATACCT CGAAAAAGCT TTTCGGATCC GGAGTTTTT TCGGAGGAGT GATCAAGACC
241	AATAGCTCAG AGCGCGAGGC GGCTCGGC TCTGCATAAA TAAAAAAT TAGTCAGCCA TGGGGCGGAG AATGGCGCGA TTATCGAGTC TCGGCTCGG CCGAGCCCG AGACGTATTT ATTTTTTTA ATCAGTCGGI ACCCGGCTC TTACCGGCTT
321	ACTGGGCGGG GAGGGAATTA TTGGCTATTG GCCATTGCAT AGCTTGTATC TATATCATAA TATGTACATT TATATTGGGT TGACCGGCC CTCCCTTAAT AACCGATAAC CGGTAAGCTA TCGAACATAG ATATAGTATT ATACATGTA ATATAACGGA
401	CATCTCCAAT ATGACCGCCA TGTGTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGTC ATTAGTTCA GTACAGGTGA TACTGGGGGT ACAACTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCGAG TAATCAAGTA
481	AGGCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCGGCCCAT TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATCCCAAT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA
561	GAGTCAATA ATGAGGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC ATTGAGTCA ATGGGTGGAG TATTTACGGT CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGGGTTAT GCGTGAAGG TAACCTGCACT TACCCACCTC ATAAATGGCA
641	AAACTGCCA CTTCGCAGTA CATCAAGTCT ATCATATGCC AAGTCGGGCC CCTATTGACG TCAATGACGG TAAATGGGCC TTTGAAGGGT GAACGGTCAT GTAGTTTACA TAGTATACGG TTCAGGGGGG GGATAACTGC AGTTACTGCC ATTTACCGGG

FIG. 7-Page 1

pcMV-delINS35

8241	AGGACAGTAT TTGGTATCTG CGCTCTGCTG AAGCAGCTTA CCTTGGGAAA AAGATTGGT AGCTCTTGAT CGGCAAAACA TCCTGTGCATA AACCATAGAC GCAGAGGAC TTGGTCAAT GGAAGCCITTT TTCTCAACCA TCGAGAAGCTA GGCGTTTCT
8321	AACCACGGCT GGTACGGGTG GTTTTTTGT TTGCAAGCAG CAGATTAGCG GCAGAAAAA AGGATCTCAA GAAGATCCCTT TTGGTGGCGA CCATCGGCAC CAAAAAACA AACCTGGTC GTCTAATGCG CGCTTTTTT TCCTAGAGTT CTCTAGGAA
8401	TGATCTTTTC TACGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTGG TCATCAGATT ATCAAAAAAG ACTAGAAAAAG ATGCCGAGA CTGGGAGTCA CCTTGGTTTT GAGTCCAATT CCCTAAAAAC AGTACTCTAA TAGTTTTTC
8481	ATCTTCACCT AGATCCCTTTT AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT CAGTAAACTT GGTCTGACAG TAGAAGTGGA TCTAGGAAAA TTTAATTTT ACTTCAAAAT TTAGTAGAT TTCAATAATA CTCATTTGAA CCAGACTGTC
8561	TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCGCCGCTC AATGGTTAGC AATTAGTCAC TCCGTGGATA GAGTGGCTAG ACAGATAAAG CAACTAGGTA TCAACGCACT GAGGGCGACG
8641	TGTAGATAAC TACGATACGG GAGGCTTAC CATCTGGCGC CAGTCTGCGA ATGATACCGC GAGACCCOAG CTCACCGGCT ACATCTATTG ATGCTATGCC CTCGCCAATG GTACACGGG GTACGACGCT TACTATGGCG CTCTGGGTGC GAGTGGCGGA
8721	CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCGC AGCCGAGAAG TGTCTCTGCA ACTTTATCCG CCTCATCCCA GCTCTAAATA GTCTTTATTT GGTGGTGGG CCTTCCCGCG TCGGTCTTC ACCAGACGT TGAATAGGC GGAGTAGGT
8801	GTCTATTAA TGTTCGGGG AAGCTAGAGT AAGTCTTGG CCAGTTAATA GTTTCGGCAA CGTTGTGGC ATTGCTACAG CAGATAATTA ACAAGGGCGC TTGCATCTCA TTCACTAAGC GGTCAATTAT CAAAGCGGT GCAACAACGG TAAAGATGC
8881	GCATCTGCT GTACGGTGG TCGTTTGGTA TGGCTTCATT CAGTCCGGT TCCCAACCAT CAAGGGCAGT TACATGATCC CGTAGCACA CAGTGGCAGC ACCAAACCAT ACCGAGTAA GTCCAGGCCA AGGGTTGCTA GTTCCGCTCA ATGACTAGG

FIG. 5-Page 15

pCMV-delINS35

7521	CGCAATTCTCT GAGTAGGTGT CATCTATTTC TGGGGGTGG GTTGGGGCAG GACAGCAAGG GGGAGGATTG GGAGACAAT GGTAACAGA CTCATCCACA GTAAGATAAG ACCCCCAACC CCACCCCGTC CTGTCTTCC CCGTCTTAAC CCTTCTGTA
7601	AGCAGGCATG CTGGGAGCT CTTCGGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTGCT TCGGTGCGG CGAGCGGTAT TCGTCCGTAC GACCCCTGGA GAAGGCGAAG GAGCGAGTGA CTGAGGAGG CGAGCCAGCA ACCCGACGCC GCTCGGCATA
7681	CAGTCACTC AAAGCGGTA ATAGGTTAT CCACAGAATC AGGGATAAC GCAGAAAGA ACATGTGAGC AAAAGGCCAG CTCGAGTGAG TTTCCGCCAT TATGCCAATA GGTGTCTTAG TCCCTATTG GGTCTTTCT TGTACACTCG TTTTCGGTTC
7761	CAAAAGGCCA GGAACCGTAA AAAGCGCGCG TTGCTGGCGT TTTTCATAG GCTCGGCCG CCTGACGAGC ATCAAAAA GTTTTCCGGT CCTTGGCAT TTTCCGGCGC AACGACGCCA AAAAGTATC CGAGCGGGG GCACTGCTCG TAGTGTCTT
7841	TCGACGCTCA ACTCAGAGGT GCGGAAACCC GACAGGACTA TAAAGATACC AGCGTTTTC CCTCGGAAGC TCCTCGTGC AGCTGCCAGT TCAGTCTCCA CCGCTTTGG CTGTCTCAT ATTCTATGG TCGCAAAGG GGGACCTTCG AGGAGCAGC
7921	GCTCTCTGT TCCGACCCCTG CCGCTTACCG GATACCTGTC GCGCTTTCTC CCTTCGGGAA GCGTGGGCT TTCTCAATGC CGACAGGACA AGGCTGGGAC GCGGAATGGC CTATGGACAG GCGGAAAGAG GGAAGCCCTT GGCACCGGA AAGACTTAC
8001	TCACGCTCTA GGTATCTCAG TTGCGGTGAG GTCTTCGCT CCAAGCTGGG CTGTGTGCAC GAAACCCCGG TTCAGCCCGA AGTGGACAT CCGTAGAGTC AAGCCACATC CAGCAAGCA GGTTCGACCC GACACAGCTG CTTGGGGGG AAGTCGGGT
8081	CCGTGCGCC TTATCCGGTA ACTATGCTCT TGACTCCAAC CCGGTAAGAC ACCACTTATC CCCACTGCCA GCAGCCACTG GGCAGCGCG AATAGGCCAT TGATAGCAGA ACTCAGGTTC GGCCTTCTG TGTGATAG CCGTCAACCT GCTCGGTGAC
8161	GTAAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGTGGC CTAACACTAGG CTACACTAGA CATTTGCTTA ATCTGTCTGC TCATACATC CGCCACCATG TCTCAAGAAC TTCACCACCG GATTGATGCC GATTGTGATCT

FIG. 5-Page 14

pCMV-delNS3

+2 6961	S P G E I N R V A A C L R K L G V P P L R A W R H R	
	CTCTCCAGGT GAATCAATA GGTGGCGC ATGCTCAGA AACTTGGG TACGGCCCTT GCGAGTTGG AGACACGGG	
	GAGAGTCCA CTTAGTTAT CCCACGGCG TACGGAGTCT TTGAAACCC ATGGCGGAA CGCTCGAAC TCTGTGGCC	
+2 7041	A R S V R A R L L A R G R A A I C G K Y L F N W A V	
	CCCAGAGGT CCGCGTAGG CTTCGCGCA GAGGAGCAG GGTGCGCAT TGTGGCACT ACCTCTCAA GTGGCGATG	
	GGGCTCGCA GCGCGATCC GAAGACCGT CTCCTCCGTC CCGACGGTAT ACACGTTCA TGGAGAAGTT GACCGTCTAT	
+2 7121	R T K L K L T P I A A A G Q L D L S G W F T A G Y S G	
	AGAAACAGC TCAAATCAC TCCAATAGG CCGCTGGCC AGTGGACTT GTCCGCTGG TTCACGGGTG CGTACAGCGG	
	TCTTGTTCG AGTTTGAATG AGGTTATCG CCGCGACCGG TCGACCTGAA CAGCCGACC AAGTGGCGAC CGATGTGGCC	
+2 7201	G D I Y H S V S H A R P R W I W F C L L L A A G V	
	GGAGACATT TATCACAGG TGCTCATGC CCGCGCCCGC TGATCTGT TTTGCCTACT CCTGTCTCT GAGCGGTAG	
	CCCTCTCTAA ATAGTGTGC ACAGTAGG GCGCGGGCGC ACTAGACCA AAGCGGATG GACGCAACGA CGTCCCATC	
+2 7281	G I Y L L P N R	
	GCACTACCT CCTCCCAAC CGATGAAGT TGGGTAAAC ACTCCGGCT AAAAAAATA AAAAATCTAG AAAGGGCGC	
	CGTAGATGA GGAGGGGTG GCTACTTCA ACCCATTTG TGAGGCGGA TTTTTTTT TTTTATGTC TTTCGCGCG	
BamHI MluI		

+2 7361	CAAGATATCA AGGATCACT AGCGTTAGA GTCGGTGTG CAGCCTCGAC TTGSCCTTCT AGTTGCCAGC CATCTGTCT	
	GTCTATAGT TCCTAGTGA TGGCAATCT CGAGCGACTA GTCCGAGTG ACACGGAAGA TCAACGGTGC GTAGACAACA	
+2 7441	TTGCCCTCC CCGTGCCTT CCTTGACCT GGAAGTGGC ACTCCCACTG TCCTTTCCTA ATAAATGAG GAAATTCAT	
	AAGGGGAGG GGGCACGGAA GGAATCTGGA CTTTCACCG TGAGGGTAC AGGAAAGGAT TATTTTACTC CTTAACCTA	

FIG. 5-Page 13

pCMV-delINS35

+2 N T L T C Y I K A R A A C R A A G L Q D C T M L V C G
 6401 AACACCCTCA CTGTGATCAT CAAGGCCGG GCAGCCTETC GTCCACGATG TGCACCATGC TCGTGTGTGG
 TTGTGGGAGT GAACGATGTA GTTCGGGCC GTCCGACAG CTCGGCGTCC CGAGGTCTGT ACGTGTATCG AGCACACAC

+2 D D L V V I C E S A G V Q E D A A S L R A F T E A M
 6481 CGACGACTTA CTCGTATCT GTCAAGGCG GGGGTCCAG GAGGACGGG CGAGCCTGAG AGCCTTCACG GAGGTATGA
 GCTGCTGAAT CAGCAATAGA CACTTTCGGC CCCCAGETC CTCCTGCGCC GTCCGACTC TCGGAAGTC CCGCATATC

+2 T R Y S A P P G D P P Q P E Y D L E L I T S C S S N V
 6561 CGAGGTACTC GCGCCGCCCT GGGGACCCCG CACAACGAGA ATACGACTTG GAGCTCATAA CATCATGCTC CTCGCAACCTG
 GGTCCATGAG CCGGGGGGGA CCGCTGGGG GTCTGTGCTC TATGCTGAAC CTGAGTATT GTAGTACGAG GAGGTGAC

+2 S V A H D G A G K R V Y Y L T R D P T T P L A R A A W
 6641 TCAGTCGCC ACGACGGCG TGAAGAAGG GTCTACTACC TCACCCGTGA CCTACAAAC CCCCTCGGA GAGCTGCGTG
 AGTCACGGG TCGTCCGGG ACCTTTCTC CAGATGATGG AGTGGCACT GGTATGTTGG GGGGAGGCT CTCGACGAC

+2 E T A R H T P V N S W L G N I I M F A P T L W A R M
 6721 GGAGACAGCA AGACACACTC CAGTCAATTC CTGGCTAGG AACATAATCA TGTTCGCCC CACACTGG GCGAGGATGA
 CCTCTGCTCT TCTGTGTGAG GTCACTTAAG GACCGATCCG TTGATTAGT ACAACGGGG GTGTGACACC CCGTCTACT

+2 I L M T H F F S V L I A R D Q L E Q A L D C E I Y G A
 6801 TACTGATGAC CCAATTCCTT AGCGTCTCTTA TAGCCAGGGA CCAGCTTCAA CAGGCGCTCG ATTGCGAGAT CTACGGGGCC
 ATGACTACTG GGTAAAGAAA TCGCAGGAAT ATCGGTCCCT GTTCGAACTT GTCCGGGAGC TAAAGCTCTA GATGCGCGG

+2 C Y S I E P L D L P P I I Q R L H G L S A F S L H S Y
 6881 TGCTACTCCA TAGAACCACT GGATCTACCT CCAATCAATC AAAGACTCCA TGGCCTCAGC GCATTTTTCAC TCCACATTA
 ACGATGAGGT ATCTTGGTGA CCTAGATGGA GTTATGTAAG TTTCTGAGGT ACCGAGCTCG CGTAAAGCTC AGGTGTCAAT

FIG. 5-Page 12

pCMV-delNS35

+2 Y A A Q G Y K V L V L N P S V A A T L G F G A Y M S K
 2001 ATGCAGTCA GGGCTATAAG GTGCTAGTAC TCAACCCCTC TGTGTCTGA ACACCTGGCT TTGGTGCTTA CATGTCCAAG
 TACGTGAGT CCGGATATTC CAGCATCATG AGTTGGGAG ACAACGACCT TGTGACCGA AACACGAAT GTACAGTTTC

+2 A H G I D P N I R T G V R T I T T G S P I T Y S T Y G
 2081 GCTCATCGGA TGGATCTTAA CATCAGGACC GGGGTGAGAA CAATTACCAAC TGGAGCCCC ATCAGTACT CCACCTACGAG
 CGAGTACCCT AGCTAGGATT GTAGTCTTGG CCCCACTTCT GTTAATGTGT ACCCTCGGG TAGTGCATGA GTGGGATGCG

+2 K F L A D G G C S G G A Y D I I I C D E C H S T D A
 2161 CAAGTTCCTT GCCAGCGCG GTGTCTCGG GCGGCTTAT GACATAATAA TTGTGACGA GTGCCACTCC AGGATGCCA
 GTTCAAGGAA CCGCTGCCGC CCAGAGCCCC CCGGGAATA CTGTATTAT AAACACTGCT CACGCTGAGG TGCCTACGGT

+2 T S I L G I G T V L D Q A E T A G A R L V V L A T A T
 2241 CATCCATCTT GGGCATTGGC ACTGTCTTGG ACCAAGCAGA GACTCGGGG GCGAGACTGG TTGTGCTGG CACCGCCAGC
 GTAGGTAGAA CCGCTAACCG TGACAGGAAC TGGTCTCTCT CTGACGCCCC CGCTCTGACC AACACGAGCG GTGGCGGTGG

+2 P P G S V T V P H P N I E E V A L S T T G E I P F Y G
 2321 CCTCGGGGT CCGTCACTGT GCCCATCCC AACATCGAGG AGGTTGCTCT GTCCACCACC GGAGAGATCC CTTTITACGG
 GGAGGCCGGA GGCATGACA CGGGGTAGGG TTGTAGTCC TCCAACGAGA CAGGTGGTGG CCTCTTAGG GAAAAATGCC

+2 K A I P L E V I K G G R H L I F C H S K K K C D E L
 2401 CAAGGTATG CCCCTGAAG TAATCAAGG GGGGAGACAT CTCATCTTCT GTCAATCAAA GAAGAAGTC GACGAACCTCG
 GTTCCGATAG GGGAGGCTTC ATTAGTTCCC CCGCTCTGTA GAGTAGAAGA CACTAAATTT CTTCCTCAGC CTGCTTGAGC

+2 A A K L V A L G I N A V A Y Y R G L D V S V I P T S G
 2481 CCACAAGCT GTCCGACTG GGCATCAATG CCGTGGCGCTA CTACGGGGGT CTTGACGTGT CCGTCACTCC GACCAAGCGG
 GGGGTTTCA CCACGTTAC CCGTAGTTAC GGCACCGGAT GATGGCGCCA GAACTGCACA GGCAGTAGG CTGGTGGCGG

FIG. 5-Page 4

pcMV-deINS35

+2	G A K D V R C H A R K A V T H I N S V W K D L L E D N	
5841	GGGCAAGA CGTCCGTTC CATCCAGAA AGCGGTAA CACATCAAC TCCGTGTGA AGACCTTC GGAAGAAT	
	CCCGTTTCT GCAGGAAG GTACGGTCTT TCCGGCATG GGTGTAGTG AGGCACACT TTCTGGAAGA CCTTCTGTA	
+2	G T A C K A T A G T A C C A T C A T G G C T A A G A A C G A G G T T T T C T G C C T T C A C C T C G A G A A G G G G T C G T A G C G A G C A T T G C G T G C	
5921	GTACACAA TAGACCTAC CATCATGGCT AAGAACGAGG TTTCCTGCT TCACCTGAG AAGGGGTC GTAGCGAGC	
	CATTGGGTT ATCTGTGATG GTAGTACCGA TTCTGTCTC AAAAGACGA AGTCGGACTC TTCCCCCAG CATTCGGTGC	
+2	R L I V F P D L G V R V C E K M A L Y D V V T K L P	
6001	TCGTCTCATC GTTTCCTCG ATCTGGCGT CGCGTGTGC GAAAGATGG CTTCGTACGA CGTGTACCA AGCTCCCT	
	AGCAGATG CACAAGGGGC TAGACCGCA CGGCACAGC TTTTCTACC GAAACATGCT GCACCAATGT TTCGAGGGA	
+2	L A V M G S S Y G F Q Y S P G Q R V E F L V Q A W K S	
6081	TGGCGTGAT GGAAGCTCC TAGGATTCC AATACTCAC AGCAGCGG GTTGAATTC TCCTCCAAG GTGGAAGTCC	
	ACCGGCATA CCTTCGAGG ATGCCTAAG TTATAGTGG TCCTGTGCC CAACTTAAG AGCAGTTC CACCTTCAGG	
+2	K K T P M G F S Y D T R C F D S T V T E S D I R T E E	
6161	AAGAAACC CAATGGGTT CTCGTATGAT ACCGCTGTG TTGACTCCAC AGTCACTGAG AGCGACATCC GTACGAGGA	
	TTCTTTGG GTTACCCCAA GAGCATACTA TGGCGACGA AACTGAGTG TCAGTGACTC TCCTGTAGG CATGCTCT	
+2	A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G	
6241	GGCAATCTAC CAATGTTGT ACCTCGACC CCAAGCCGC GTGGCCATCA AGTCCCTCAC CGAGAGGCTT TATGTTGGG	
	CCGTTAGATG GTTACACAC TGGAGCTGGG GGTTCGGGC CACGGTAGT TCAGGGAGTG GCTTCGGAA ATACACCCC	
+2	G P L T N S R G E N C G Y R R C R A S G V L T T S C G	
6321	GCCCTCTTAC CAATTCAGG GGGGAACT GGGGTATCG CAGTCCCG CGGAGCGGC TACTGACAAC TAGTGTGGT	
	CGGGAGATG GTTAAGTTC CCCCTCTTGA CCGCATAGC GTCCACGGC TGCCTGGCG ATGACTGTTG ATCGACACCA	

FIG. 5-Page 11

pCMV-delINS35

+2	S	T	L	S	T	A	L	A	E	L	A	T	R	S	F	G	S	S	S	T	S	G	I	T	G	D	
5281	ATCAACCTTA	TTACTTCGCT	TGCGCGAGCT	CGGCACACAGA	AGCTTTGSCA	GCTCTCTCAAC	TTCCGCGCAT	ACGGCGGACA	TAGTTGGGAT	AGATGACGGA	ACCGGCTCGA	GGGTTGGTCT	TCGAAACCGT	CGAGGAGTTG	AAGGCGGTAA	TGCCCGCTGT											
+2	N	T	T	T	S	S	E	P	A	P	S	G	C	P	P	D	S	D	A	E	S	Y	S	S	M	P	P
5361	ATACGACAAC	ATCCTCTGAG	CCGCGCCCTT	CTGGCTGCC	CCCGCACTCC	GACGCTGACT	CCTATTCTC	CATGCCCCCC	TATGCTGTIG	TAGGAGACTC	GGGCGGGGAA	GACCGACGGG	GGGCTGAGG	CTCGCACTCA	GGATAAGGAG	GTACGGGGGG											
+2	L	E	G	E	P	G	D	P	D	L	S	D	G	S	W	S	T	V	S	S	E	A	N	A	E	D	V
								BamHI																			
5441	CTGAGAGGGG	AGCCTGGGGA	TCCGGATCTT	AGCGACGGGT	CATGGTCAAC	GGTCAAGTAGT	GAGGCCAACG	CGGAGGATGT	GACCTGCCCC	TGGGACCCCT	AGGCCTAGAA	TCGCTGCCCA	GTACCAAGTTG	CCAGTCATCA	CTCCGGTTGC	GCCTCCTACA											
+2	V	C	C	S	M	S	Y	S	W	T	G	A	L	V	T	P	C	A	A	E	E	Q	K	L	P	I	
5521	CGTGTGCTG	TCAATGTCTT	ACTCTTGAC	AGGGGCACTC	GTACCCCGGT	CGCGCGGGA	AGAACAGAAA	CTGCCCATCA	GCACACGACG	AGTTACAGAA	TGAGAACCTG	TCCGCGTGAG	CAGTGGGGCA	CGCGGGCGCT	TCCTGTCTTT	GACGGGTAGT											
+2	N	A	L	S	N	S	L	L	R	H	H	N	L	V	Y	S	T	T	S	R	S	A	C	Q	R	Q	K
5601	ATGCACTAAG	CAACTCGTTG	CTACGTCACC	ACAATTGGT	GTATTCCACC	ACCTCACGCA	GTGCTTGCCA	AAGCGAGGAG	TACGTGATTC	GTGAGGCAAC	GTGAGAGTGG	TGTTAAACCA	CATAAGGTGG	TGAGTGCCT	CACGACGGT	TTCCGTCTTC											
+2	K	V	T	F	D	R	L	Q	V	L	D	S	H	Y	Q	D	V	L	K	E	V	K	A	A	A	S	K
5681	AAAGTCACAT	TTGACAGACT	GCAAGTTCTG	GACAGCCATT	ACCGAGCAGT	ACTCAAGGAG	GTATAAGCAG	CGCGCTCAA	TTTCACTGTA	AACCTCTCTG	CGTTCAAGAC	CTGTGGGTAA	TGTCCTGCA	TGAGTTCTCT	CAATTTCGCT	CGCGCAGTTT											
+2	V	K	A	N	L	L	S	V	E	E	A	C	S	I	T	P	P	H	S	A	K	S	K	F	G	Y	
5761	AGTGAAGGCT	AACCTGTGAT	CGGTAGAGA	AGCTTGCAGC	CTGACGCCC	CACATCTCAG	CAATCAAG	TTTGGTTATG	TCACTTCCGA	TTGAACGATA	GGCATCTCT	TGAGACCTCG	GACTGCGGGG	GTGTGAGTCG	GTTTAGGTTT	AAACCAATAC											

FIG. 5-Page 10

pcMV-delINS35

+2	L	H	E	Y	P	V	G	S	Q	L	P	C	E	P	D	V	A	V	L	T	S	M	L	T	D		
4721	CTCCACGAAT	ACCGGTAGG	GTGCGAATTA	CCTTGGGAGC	CGGAACGGGA	CGTGGCCGTG	TTGAGCTCCA	TGCTCACTGA	GAGGTGCTTA	TGGGCGCATCC	CAGCCTTAAT	GGAACGCTCG	GCCTTGGCCT	GCACCGGCAC	AACCTGCAGGT	ACCACTGACT											
+2	P	S	H	I	T	A	E	A	A	G	R	R	L	A	R	G	S	P	P	S	V	A	S	S	A		
4801	TCCCTCCCAT	ATAACAGAG	AGGCGCGCG	GGCAAGGTG	CGGAGGGAT	CACCCGCCCTC	TGTGGCCACC	TCTCGCGTA	AGGAGGGTA	TATTGTGCTC	TCGCGCGCC	CGCTTCCAA	CGCTCCCTTA	GTGGGGGGAG	ACACCGGTG	AGGAGCGCA											
+2	S	Q	L	S	A	P	S	L	K	A	T	C	T	A	N	H	D	S	P	D	A	E	L	I	E	A	N
4881	CCGAGTATC	CGTCCATCT	CTCAAGGCA	ATTGACCGC	TAAACATGAC	TCCCTGTATG	CTGAGCTCAT	AGAGGCCAAC	CGGTGATAG	GGGAGGTAGA	GAGTTCCGTT	GAACCTGGCG	ATTGGTACTG	AGGGGACTAC	CAGTCCAGTA	TCTCCGGTTT											
+2	L	L	W	R	Q	E	M	G	G	N	I	T	R	V	E	S	E	N	K	V	V	I	L	D	S	F	D
4961	CTCCTATTGA	GCGAGGAGG	ACGAGCGGA	GATCTCCGTA	CCCGAGAAA	TCTGTCGGAA	GTCTCGGAGA	TTCCGCCAGG	GAGGATACCT	CCGTCTCTTA	CCGCGCGTTG	TAGTGTGCC	AACCTCAGTCT	TTTGTTCAC	CACCTAAGACC	TCAGGAAGCT											
+2	P	L	V	A	E	D	E	R	E	I	S	V	P	A	E	I	L	R	K	S	R	R	F	A	Q		
5041	TCGCGTTGTG	GCGGAGGAG	ACGAGCGGA	GATCTCCGTA	CCCGAGAAA	TCTGTCGGAA	GTCTCGGAGA	TTCCGCCAGG	AGCGGAACAC	CGCCTCTCC	TGCTCGCCTC	CTAGAGGCAI	GGCGTCTTT	AGGACGCTT	CAGAGCCTCT	AAGCGGGTCC											
+2	A	L	P	V	W	A	R	P	D	Y	N	P	P	L	V	E	T	W	K	K	P	D	Y	E	P	P	V
5121	CCCTGCGCGT	TTGGGCGCGG	CGGAGCTATA	ACCCCGCGT	AGTGAGAGG	TGGAAGAGC	CCGACTACGA	ACCACTGTG	GGGACGGGCA	AACCGCGCC	GGCCTGATAT	TGGGGGGCA	TCACCTCTGC	ACCTTTTTCG	GGCTGATGCT	TGCTGGACAC											
+2	V	H	G	C	P	L	P	P	K	S	P	P	V	P	P	P	R	K	K	R	T	V	V	L	T	E	
5201	GTCCATGCTG	CGCCGCTTCC	ACCTTCAAG	TCCCTCTCTG	TGCTTCCGCC	TCGGAAGAG	CGGACGCTGG	TCCTCACTGA	CAGGTACCGA	CGGCGGAAG	TGGAGTTTC	AGGGGAGGAC	ACGAGGGCGG	AGCCTTCTTC	GCCTGCCACC	AGGAGTCACT											

FIG. 5-Page 9

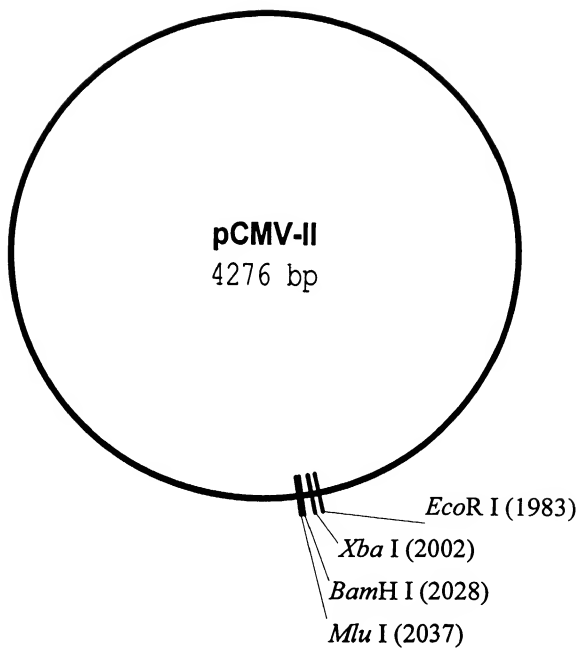


FIG. 6

pCMV-delNS35

8961	CCCATGTTGT GCAAAAAGC GGTAGCTCC TTGGTCCTC CGATCGTGT CAGAAAGTAAG TTGGCCGCG AGTGTATCACT GGGTACAACA CGTTTTTTTCG CCAATCGAGG AAGCCAGGAG GCTAGCAACA GTCTTCAITC AACGGGGT CACAATAGTGA
9041	CATGGTTATG GCAGCACTGC ATAAATCTCT TACTGTCTAT CCATCCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA GTACCAATAC CGTCGTGACG TATTAAGAGA ATGACAGTAC GGTAGGCAIT CTACGAAAAG ACACTGACCA CTCATGAGTT
9121	CCAAGTCATT CTGAGATAG TGTATGGCG GACCGAGTTG CTCTTGCCG GGTCAATAC GGGATAATAC CGCGCCACAT GGTTCAGTAA GACTCTTATC ACATACGCG CTGGCTCAAC GAGAACGGGC CCGACTTATG CCTATTATG CGCGGGTGA
9201	AGCACAACCT TAAAAGTGT CATCAATTGGA AAACGTTCTT GGGGGCGAAA ACTCTCAAG ATCTTACCGC TGTTCAGATC TCGTCTTGAA ATTTTCACGA GTAGTAACCT TTGCAAGAA GCCCGCTTT TGAGAGTTCC TAGAATGGG CAACTCTAG
9281	CAGTTGATG TAACCCACTC GTGCACCCAA CTCATCTTCA GCATCTTTTA CTTTCACCG CGTTTCTGG TGAGCAAAA GTCAAGTAC ATTGGGTGAG CACTGGGTT GACTAGAACT CGTAGAAAT GAAAGTGTC GCAAGACCC ACTCGTTTT
9361	CAGGAAGCA AAATGCCGA AAAAAGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCT TTTTCAATAT GTCTTCTGTT TTACGGGT TTTTCCCTT ATTCCGCTG TGCTTTACA ACTTATGAGT ATGAGAAGCA AAAAGTTATA
9441	TATTCAAGCA TTTATCAGG TTATTGCTC ATGACCGAT ACATATTGA ATGATTTAG AAAATAAAC AAATAGGGT ATAACTTGT AATAGTCC AATAACAGAG TACTCGCTA TGATAAAT TACATAATC TTTTATTG TTTATCCCA
9521	TCGGCGACA TTTCCCGAA AAGTGCACC TGACGTCTAA GAAACATTA TTATCATCAG ATTAACCTAT AAAATAGGC AGGGCGGT AAAGGGCTT TTACGGTGG ACTGCAGAT CTTTGCTAT AATAGTACTG TAATTGGAIA TTTTATCCG
9601	GTATCAGGAG GGCCTTCTG C CATAGTGT C GGGAAAGCA G

FIG. 5-Page 16

pCMV-delNS35

+2	I	S	S	E	C	T	T	P	C	S	G	S	L	R	D	I	W	D	W	I	C	E	V	L	S	D	
4161	TAAGCTCGGA	GTGTACCACT	CCATGCTCCG	GTTCCTGGT	AAGGCATC	TGGGACTGGA	TATGCGAGT	GTTAGCGAC	ATTGAGGCT	CACATGGTGA	GGTAGAGGC	CAAGGACCGA	TTCCCTGTAG	ACCTGA	CACT	ATACGCTCA	CAATCGCTG										
+2	F	K	T	W	L	K	A	K	L	M	P	Q	L	P	G	I	P	F	V	S	C	Q	R	G	Y	K	G
4241	TTTAAGACCT	GGGTAAAGC	TAAGTCATG	CCACAGCTGC	CTGGGATCCC	CTTTCTGTCC	TGCCAGGCGG	GGTATAAGG	AAATTTCTGGA	CCGATTTTCG	ATTGCACTAC	GGTGTGAGG	GACCCTAGGG	GAAACACAGG	ACGCTGCCG	CCATATTC											
+2	V	W	R	G	D	G	I	M	H	T	R	C	H	C	G	A	E	I	T	G	H	V	K	N	G	T	
4321	GGTCTGCGA	GGGACGGGA	TCATGCACAC	TGCTGCCAC	TGTGGAGCTG	AGATCACTGG	ACATGTCAAA	AACGGGAGGA	CCAGACCGCT	CCCCTGCCGT	AGTACGTGTG	AGCGACGGTG	ACACCTCGAC	TCTAGTGACC	TGTACAGTTT	TTCGCTGCT											
+2	M	R	I	V	G	P	R	T	C	R	N	M	W	S	G	T	F	P	I	N	A	Y	T	T	G	P	C
4401	CTCAGGATGT	CGGTCTAGG	ACCTGCAGGA	ACATGTGAG	TGGGACCTTC	CCCATTAATG	CCTACACAC	GGGCCCTGT	ACTCCTAGCA	GCCAGGATCC	TGGACGTCT	TGTACACCTC	ACCTGGAAG	GGTAATTAC	GGATGTGCTG	CCCGGGGACA											
+2	T	P	L	P	A	P	N	Y	T	F	A	L	W	R	V	S	A	E	E	Y	V	E	I	R	Q	V	G
4481	ACCCCTCTC	CTGCGCGAA	CTACAGCTC	CGCTATGGA	GGTCTCTGC	AGAGGAATAC	GTGGAGATAA	GGCAGTGGG	TGGGGGAAG	GACGGGGCTT	GATCTGCAAG	CCCGATACCT	CCGACAGAGC	TCTCCTTATG	CACCTCTATT	CCGTCCACCC											
+2	D	F	H	Y	V	T	G	M	T	T	D	N	L	K	C	P	C	Q	V	P	S	P	E	F	F	T	
4561	GGATCTCCAC	TACGTGACGG	GTATGACTAC	TGACAACTTT	AAATGCCGT	CGCAGGTCCG	ATCGCCGAA	TTTTTCACAG	CCTCAAGGTG	ATGCATGCC	CATACTGATG	ACTGTAGAA	TTTACGGGGA	CGGTCCAGGG	TAGCGGGCTT	AAAAAGTGTG											
+2	E	L	D	G	V	R	L	H	R	F	A	P	P	C	K	P	L	L	R	E	E	V	S	F	R	V	G
4641	AAATTGACGG	GGTGGCCCTA	CATAGTTTG	CGCCCGCTG	CAAGCCCTTG	CTGCGGGAGG	AGGTATCAT	CAGAGTAGGA	TTAACCTGCC	CCACGGGAT	GTATCCAAAC	GCGGGGGGAC	GTTTGGGGAAC	GAGGCCCTCC	TCCATAGTAA	GTCTCATCT											

FIG. 5-Page 8

pCMV-delINS35

1361	CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT CACAGGAGCT CTGTATTTTT ACAGATGGG GTCCATTATAT GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTCA GTGTGCTGA GACATAAAA TGTCTTACCC CAGTAATAA
1441	TATTACAAA TTCACATATA CAACAAGCC GTCCCCCGTG CCGCGAGTTT TTATTAAACA TAGCGTGGA TCTCCGACAT ATAAATGTT AAGTGATAT GTTCTCGG CAGGGGCGAC GGGCGTCAAA AATAATTTGT ATGCCACCT AGAGGCTGA
1521	CTCGGTAAG TGTTCGGAC ATGGGCTCTT CTCGGTAGC GGGGAGCTT CCACATCGA GGCCTGCTCC CATCCGTCOA GAGCCATGC ACAAGGCTG TACCGAGAA GAGGOCATCG CCGCTCGAA GGTGTAGCT CCGGACCAGG GTAGGCGGT
1601	CGGCTCATG CTCGCTCGC AGTCTCTTG TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CAGCACCAAC CGCCGAGTAC CAGCGAGGCG TCGAGGAAG AGGATTGTCA CTCGGTCT GAATCCGTGT CGTGTTACGG GTGGTGGTGG
1681	AGTGTGCGC ACAAGGCGT GCGGTAGG TATGTCTG AAAATCAGT CCGAGATTGG GCTCGCACCT GACGCGAGAT TCACACGGCG TGTTCGGCA CCGCATCCC ATACAGAC TTITACTGA GCCTCTAAC CGAGCGTGA CTGCGCTA
1761	GGAAGACTTA AGGCAGCGC AGAAGAAGT GCAGCGAGCT GAGTTGTTGT ATTCTGATA GAGTCAGAGG TAACTCCCT CCTTCTGAAT TCCGTCGCG TCTTCTCTA CGTCCGTCGA CTCACAACA TAAGACTATT CTCAGTCTCC ATTGAGGGA
1841	TGGGTGCTG TTAACGGTG AGGCGAGTGT AGTGTGACA GTACTGTTG CTGCGCGCG GCGCACCGA CATAAATAGT ACGCCAGAC AATTGCCACC TCCGCTACA TCAGACTGT CATGACAA CAGCGGCGG CCGGTGCTCT GTATTATGA
+2	
1921	GACAGACTAA CAGACTGTTT CTTTCATGG GTCTTTCTG CAGTCACCGT CGTGACCTTA AGAATTCAAC ATGGGTGAT CTGTCTGATT GTCTGACAAG GAAAGGTACC CAGAAAAGC CTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGACGTA

M A A

EcoRI

FIG. 5-Page 3

pCMV-delNS35

641	AAAGTGGCCA CTGGCAGTA CATCAAGTCT ATCATATGCC AAGTCGGCC CCTATTGACG TCAATGACGG TAAATGGGCC TTTGACGGGT GAACGGTCAT CTAGTTCACA TAGTATACGG TTCAGCGGGG GGATAACTGC AGTTACTGCC ATTTACCGGG
721	GCCTGGCATT ATGCCAGTA CATGACCTTA CGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CGGACCGTAA TACGGGTCTAT GTACTGGAAT GCCTGAAAG GATGAACGGT CATGTAGATC CATATCACT ACGGATAATG
801	CATGGTGATG ATGCCAGTA CATGACCTTA CGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC GTACCACTAC GCGGAGTTC GTACTGGAAT GCCTGAAAG GATGAACGGT CATGTAGATC CATATCACT ACGGATAATG
881	CATGGTGATG ATGCCAGTA CATGACCTTA CGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC GTACCACTAC GCGGAGTTC GTACTGGAAT GCCTGAAAG GATGAACGGT CATGTAGATC CATATCACT ACGGATAATG
961	TTGACGCTAA TGGGAGTTTG TTTTGGCACC AAAATCAAGG GGAATTTTCCA AAATGTCGTA ATAACCCCGG CCGGTTGACG AACTGCAGTT ACCCTCAAAAC AAAACCGTGG TTTTACTTGC CCTGAAAGGT TTTACAGCAT TATTGGGGGG GGGCAACTGC
1041	CAAATGGCGG GTAGCGGTGT ACGGTGGGAG GTCTATATAA GCAGAGTTCG TTTAGTGAAC CGTCAGATCG CCGTGGAGACG GTTTACCGCG CATCGGACA TGCCACCGTC CAGATATATT CGTCTCGAGC AAATCACTTG CGACTCTAGC GGAACCTCTGC
1121	CGATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGAC CGATCCAGCC TCCGCGGGCG GGAACGGTGC ATTGGAACGC GGTAGGTGG ACAAAACTCG AGGTATCTTC TGTGCGCCCTG CTAAGTTCGG AGGCGCGGGC CCTTGGCAGC TAACTTTGCG
1201	GGATTCCCGG TGCCAAGAGT GACCTAAGTA CGCCTATAG ACTCTATAG CACACCCCTT TGGCTCTTAT GCATCCTATA CCTAAGGGGC ACGGTTCTCA CTGCATTAT GCGGATATC TGAGATATCC GTCTGGGAA ACCGAGAATA CGTACGATAT
1281	CTGTTTCTTG CTGGGGCT ATACACCCCG GTCCTTATG CTATAGGTGA TGGTATAGCT TACGCTATAG GTGTGGGTTA GACAAAACCG GAACCCCGGA TAUTGGGGG CGAGGAATAC GATATCACT ACCATATCGA ATCGGATATC CACACCAAT
1361	TTGACCATTA TTGACCACTC CCCTATTGGT GACGATACCT TCCATTACTA ATCCATAACA TGGCTCTTTG CCACAACTAT AACTGCTAAT AACTGCTGAG GGGATAACCA CTGCTATGAA AGGTATGAT TAGGTATTGT ACCGAGAAC GGTCTTGATA

FIG. 5-Page 2

pCMV-delNS35

+2	L	S	T	L	P	G	N	P	A	I	A	S	L	M	A	F	T	A	A	V	T	S	P	L	T	T	
3601	CTTGTC	CAACG	CTGC	TGGTA	ACCCG	GCAT	TGCTT	CAATTG	ATGGCTTTTA	CAGCTGCTCT	CACGACGCCA	CTAACCACTGA	GAACAGTTGC	GACGGACCAT	TGGGGCGGTA	ACGAAGTAAC	TACCGAAAT	GTCCACGACA	GTGGTCGGGT	GATTGGTGAAT							
+2	S	Q	T	L	L	F	N	I	L	G	G	W	V	A	A	Q	L	A	A	P	G	A	A	T	A	F	V
3681	GCCAAACCT	CCTCTTCAAC	ATATTGGGG	GGTGGGTGGC	TGCCAGCTC	GCGGCCCGCG	GTGCGGCTAC	TGCTTTTGTG	CGGTTTGGGA	GGAGAAGTTG	TATAACCCCG	CCACCCACCG	ACGGGTCCGAG	CGGCGGGGGC	CACGGCGATG	ACGGAACAC											
+2	G	A	G	L	A	G	A	A	I	G	S	V	G	L	G	K	V	L	I	D	I	L	A	G	Y	G	A
3761	GGCGTGGCT	TAGCTGGCG	CGCCATCGCG	AGTGTGGAC	TGGGGAAGGT	CCTCATAGAC	ATCCTTGCAG	GGTATGGCGC	CCGGACCGGA	ATCGACCCCG	CGGTAAGCG	TCACAACCTG	ACCCCTTCCA	GGAGTATCTG	TAGGAACGTC	GCATACCGCG											
+2	G	V	A	G	A	L	V	A	F	K	I	M	S	G	E	V	P	S	T	E	D	L	V	N	L	L	
3841	GGCGTGGCG	GGAGCTCTTG	TGGCATTCAA	GATCATGAC	GGTGAGGTCC	CCTCCACGGA	GGACCTGGTC	AATCTACTGC	CCCGCACCGC	CCTCGAGAAC	ACCGTAAGTT	CTAGTACTCG	CCACTCCAGG	GGAGGTCCCT	CCTGGACCAG	TTAGATGACG											
+2	P	A	I	L	S	P	G	A	L	V	V	G	V	V	C	A	A	I	L	R	R	H	V	G	P	G	E
3921	CGGCACTCT	CTCGCGCGGA	GCCTCTGTAG	TGGCGGTGGT	CTGTGACGCA	ATACTCGGCC	GGACGTTGG	CCCGGGCGAG	GGCGGTAGGA	GAGCGGGCCT	CGGGAGCATC	AGCGGACCA	GACAGCTCGT	TATGACGGG	CCGTGCAACC	GGCGCCGCTC											
+2	G	A	V	Q	W	M	N	R	L	I	A	F	A	S	R	G	N	H	V	S	P	T	H	Y	V	P	E
4001	GGGCGAGTGC	ACTGCATGAA	CGGCTCGATA	GCCTTCGCCT	CCCGGGGGAA	CCATGTTTCC	CCGACGCACT	ACGTGCCGGA	CCCGGTACG	TCACCTACTT	GGCGGACTAT	CGGAAGCGGA	GGGCCCCCTT	GGTACAAAGG	GGGTGCTGTA	TGCACGGCCT											
+2	S	D	A	A	A	R	V	T	A	I	L	S	S	L	T	V	T	Q	L	L	R	R	L	H	Q	W	
4081	GAGGATGCA	GCTCGCGCGG	TCACTGCCAT	ACTCAGCAGC	CTCACTGTAA	CCGAGCTCCT	GAGCGCACTG	CACCACTGGA	CTCGCTACGT	CGACGGGGCG	AGTGAGGTA	TGAGTCTCTG	GAGTGACATT	GGGTGAGGGA	CTCCGCTGAC	GTGCTACCT											

FIG. 5-Page 7

pCMV-delNS35

1	TCGGCGCTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT AGCGCGCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGCG CTCTGCCAGT GTCGAACAGA CATTCGCCTA
81	CGCGGGAGCA GACAAGCCGG TCAGGCGCG TCAGCGGTG TTGGCGGGTG TCGGGGGTGG CTTAACTATG CGGCATCAGA CGGCGCTCGT CTGTTCGGGC AGTCCCGCG AGTCCCGCG AGTCCCGCG AACCGCCAC AGCCCGACC GAAITGATAC GCGGTAGTCT
161	GCAGATTGTA CTGAGAGTGC ACCATATGAA GCTTTTGGCA AAAGCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG CGTCTAACAT GACTCTCAG TGGTATACTT CGAAAAACGT ITTCGGATCC GGAGGTTTT TCGGAGGAGT GATGAAGACC
241	AATAGCTCAG AGGCGCGAGG GGCCTCGGC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGGGGCGGAG ATTGGGCGGA TTATCGAGTC TCCGGCTCCG CCGGAGCGCG AGAGTATT ATTTTTTTA ATCAGTCGGT ACCCGGCTC TTACCGGCT
321	ACTGGCGGG GAGGGAATTA TTGGCTATTG GCCATTGCAT AGTTGTATC TATATCATAA TATGTACATT TATATTGGCT TGACCGCGCC CTCCTTTAAT AACCGATAAC CGGTAACGTA TCCACATAG ATATAGTATT ATACATGTA ATATAACCGA
401	CATCTCCAAAT ATGACCGCCA TGTTGACATT GATTATTGAC TAGTTATTA TAGTAATCAA TTACGGGGTC ATTAGTTCAT GTACAGGTTA TACTGGGGGT ACACTGTAA CTAATAACTG ATCAATAAIT ATCATTAGT AATGCCCGAG TAATCAAGTA
481	AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCGCGC TGGCTGACCG CCCAACGACC CCCGCCATT TGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACGGGCGG ACCGACTGCC GGGTTGCTGG GGGCGGGTAA
561	GAGTCAATA ATGACGTATG TTCCCATACT AACGCCAATA GGACTTTCC ATTGACGTCA ATGGGTGGAG TATTACGGT CTGCACTTAT TACTGCATAC AAGGTAATCA ITTCGGTTAT CCCTGAAAG TAACTGCCAG TACCCACCTC ATAAATGCCA

StuI
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FIG. 5-Page 1

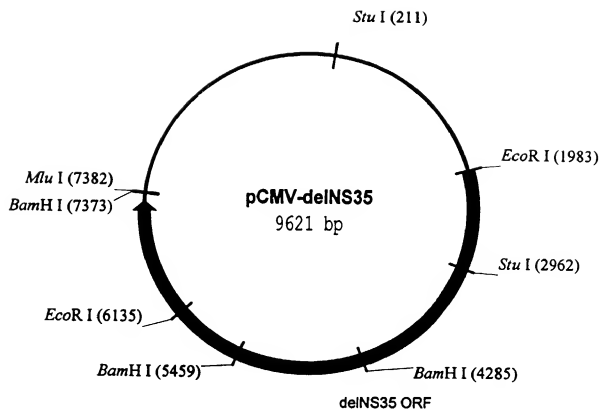


FIG. 4

pCMV-delNS35

+2	A	T	V	C	A	R	A	Q	A	P	P	P	S	W	D	Q	M	W	K	C	L	I	R	L	K	P	T
3041	GC	CA	CG	T	GT	GC	CT	AG	GC	TCA	AG	CC	CC	T	GC	T	GG	CA	CA	AG	T	TT	CA	T	T	CC	GC
	CG	GT	GG	C	A	CG	AT	CC	CG	AG	GG	GG	GG	A	CG	AT	CC	CA	CT	T	C	A	A	A	CG	GC	GC
+2	L	H	G	P	T	P	L	L	Y	R	L	G	A	V	Q	N	E	I	T	L	T	H	P	V	T	K	
3121	CC	TC	CA	T	GG	CG	CA	CC	TC	GT	AT	AC	AG	CT	GG	CG	CT	GT	T	CA	CA	AG	AT	GC	CA	CA	
	GG	AG	T	ACC	CG	TT	T	GG	GG	AC	GA	T	GC	TC	CG	CG	GA	CA	AG	T	T	AG	T	GG	GA	CT	
+2	Y	I	M	T	C	M	S	A	D	L	E	V	T	S	T	W	V	L	V	G	G	V	L	A	A	L	
3201	AC	AT	CA	T	GC	AT	GC	TC	GG	CG	AC	T	GG	AG	TC	GC	TC	AC	AG	CA	CT	GC	T	GC	T	GC	
	T	GT	AG	T	ACT	T	AG	CT	GC	CG	GG	AC	TC	CA	AG	CA	CT	GC	TC	GG	AC	CA	CG	CA	CA	CA	
+2	A	A	Y	C	L	S	T	G	C	V	V	I	V	G	R	V	V	L	S	G	K	P	A	I	I	P	D
3281	GC	CG	CG	T	ATT	GC	CT	GT	CA	AC	AG	GT	CG	CT	GC	TC	AT	GC	TC	GG	AG	GG	GT	CT	GC	TC	
	CG	CG	CG	CA	TAA	CG	CA	AG	T	T	CG	CG	CG	CA	AG	CA	CT	GC	TC	GG	AG	GG	GT	CT	GC	TC	
+2	R	E	V	L	Y	R	E	F	D	E	M	E	E	C	S	Q	H	L	P	Y	I	E	Q	G	M	M	
3361	C	AG	GA	AG	TC	TA	CG	AG	AG	T	T	CG	AT	GA	C	AT	GA	CG	TC	CA	T	CA	CG	TC	CA		
	GT	CC	CT	TC	AG	AT	GG	CT	C	A	AG	T	CT	CT	C	A	G	A	G	AT	CG	CA	T	CA	CG	TC	
+2	L	A	E	Q	F	K	Q	K	A	L	G	L	L	Q	T	A	S	R	Q	A	E	V	I	A	P	A	V
3441	TC	CG	CG	AG	CA	GT	TA	CG	AG	CA	AG	CG	CG	TC	GC	AT	CG	CA	AG	CG	CA	AG	CG	CA	AG	CG	
	AG	CG	CG	CT	CG	CA	AG	T	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	
+2	Q	T	N	W	Q	K	L	E	T	F	W	A	K	H	M	W	N	F	I	S	G	I	Q	Y	L	A	G
3521	C	A	G	A	C	A	A	A	C	T	T	C	G	A	A	C	T	T	C	A	C	A	A	A	A	A	A
	GT	CT	GG	TT	GA	CG	GT	TT	TT	GA	GT	CT	GG	AA	AC	CG	GT	TT	GA	AT	AT	AT	AT	AT	AT	AT	

FIG. 5-Page 6

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+2	D	V	V	V	V	A	T	D	A	L	M	T	G	Y	T	G	D	F	D	S	V	I	D	C	N	T	C
2561	GATGTTGTG	TGTTGGCAAC	CGATGCGCTC	ATGACGGGT	ATACGGCGA	CTTCGACTCG	GTGATAGACT	GCATATACCG	CACTATCTGA	GCTTATGACG																	
	CTACAACAGC	AGCAGCGTTG	GCTACGGGAG	TACTGGCCGA	TATGGCCGCT	GAAGCTGAGC	CACATCTGA	GCTTATGACG																			
+2	V	T	Q	R	R	G	R	T	G	R	G	K	P	G	I	Y	R	F	V	A	P	G	E	R	P	S	G
2641	TGTCACCCAG	ACAGTCGATT	TCAGCCCTGA	CCCTACCTTC	ACCAITGAGA	CAATCAGGCT	CCCCGAAGAT	GCTGTCTCCG																			
	ACAGTGGGTC	TGTCAGCTAA	AGTCGGAAC	GGGATGGAAG	TGTAACCTCT	GTTAGTCGGA	GGGGTTCTA	CGACAGAGGG																			
+2	R	T	Q	R	R	G	R	T	G	R	G	K	P	G	I	Y	R	F	V	A	P	G	E	R	P	S	G
2721	GCATCTCAACG	TGGGGCAGG	ACTGGGAGG	GGAAGCCAGG	CATCTACAGA	TTTGTGGGAC	CGGGGAGGG	CCCTCTCCGG																			
	CGTGAGTTGC	AGCCCCGTCC	TGACCGTCCC	CCTTCGGTCC	GTAGATGCT	AAACACCGTG	GCCCCCTCGC	GGGGAGGCGG																			
+2	M	F	D	S	S	V	L	C	E	C	Y	D	A	G	C	A	W	Y	E	L	T	P	A	E	T	T	V
2801	ATGTTGCACT	CGTCGTCTCT	CTGTGAGTGC	TATGACGAG	GCTCTGCTTG	GTATGAGCTC	ACGCCCGCGG	AGACTACAGT																			
	TACAAGCTGA	GGAGGCAGGA	GACACTCAGG	ATACTGGCTC	CGACACGAAC	CATACTCGAG	TGGGGGCGG	TCTGATGTCA																			
+2	R	L	R	A	Y	M	N	T	P	G	L	P	V	C	Q	D	H	L	E	F	W	E	G	V	F	T	StuI
2881	TAGGCTACGA	GCCTACATGA	ACACCCCGGG	GCTTCCCGTG	TGCCAGGACC	ATCTTGAATT	TTGGGAGGGC	GTCTTTTACAG																			
	ATCCGATGCT	CCCATGTAAT	TGTGGGGCCC	GGAAGGCGAC	ACGGTCTCTG	TAGAACTTAA	AACCTCCCGG	CAGAAATGTC																			
+2	G	L	T	H	I	D	A	H	F	L	S	Q	T	K	Q	S	G	E	N	L	P	Y	L	V	A	Y	Q
	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
2961	GCCTCACTCA	TATAGATGCC	CACCTTCTAT	CCCAGACAAA	GGAGATGGG	GAGAACCTTC	CTTACTCGGT	AGCGTACCAA																			
	CGGAGTGACT	ATATCTACGG	GTGAAGAATA	GGGTCTGTTT	CGTCTCACC	CTCTTGGGAG	GAATGGACCA	TGCGATGGTT																			

FIG. 5-Page 5

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8961 CCCATCTTGT GCAAAAAGC GGTAGCTCC TTCGGTCTC GATCGTTGT CAGAAGTAAG TTGGCGGCAG TGTATCACT
GGGTACAACA CGTTTTTCG CCAATCAGG AAGCCAGGAG GTAGGAACA GTCTTCATTC AACCGGCGT ACAATAGTGA

9041 CATGGTATG GCAGCACTGC ATAATTCTCT TACTGTCA TG CATCGGTAA GATGCTTTC TGTGACTGCT GACTACTCAA
GTACCAATAC CGTCGTGAGG TATTAAAGA ATGACAGTAC GGTAGGCATT CTACGAAAAG ACATGACCA CTUATGAGIT

9121 CGAAGTCATT CTGAGATAG TGTATGCGC GACCGAGTGT CTCTTCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT
GGTTCAGTAA GACTCTTATC ACATACGCG CTGGCTCAAC GAGACGGGC CGCAGTTATG CCTATTATG GCGCGGTGA

9201 AGCAGAACTT TAAAGTCTT CATCATTTGA AAACGTTCTT CGGGGCGAAA ACTCTCAAG ATCTTACCGC TGTGAGATC
TCGCTTTGAA ATTTTCAGA GTAGTAACCT ITTGCAAGAA GCGCCGCTTT TGACAGTTCC TACAATGGCG ACAACTTAG

9281 CAGTTGCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAA
GTCAAGCTAC ATTGGGTGAG CACGTGGGTT GACTAGAAGT CGTAGAAAAT GAAACTGCTC GCAAAAGCCC ACTCGTTTTT

9361 CAGCAAGGCA AAATGCCGA AAAAAGGAA TAAAGGGGAC ACGAAATGT TGAATACTCA TACTCTTCTT TTTTCAATAT
GTGCTTTCGT TTTACGGGGT TTTTCCCTT ATTCCGCTG TGCCTTTACA ACTTATGAGT ATGAGAAGGA AAAAGTTATA

9441 TATTGAAGCA TTTATCAGG TTAATGCTC ATGACCGAT ACATATTTCA ATGTAATTTAG AAAATAAAC AAATAGGGT
ATAACTTCTG AAATAGTCCC AATAACAGAG TACTCGGCTA TGTATAACT TACATAAATC TTTTATTG TTTATGCCA

9521 TCCGGGACA TTTCCCGGAA AAGTGCCACC TGAGTCTAA GAAACATTA TTATCATGAC ATTAACCTAT AAAATAGCG
AGGCGCGTGT AAAGGGGCTT TTACGGTGG ACTGCAGATT CTTTGGTAAT AATAGTACTG TAATTGGATA TTTTATCGG

9601 GTATCAGGAG GCGCTTTCGT C
CATAGTCTC CGGAAAGCA G

FIG. 3-Page 16

pCMV-NS35

8241	AGGACAGTAT TTGTAATCTG CGCTCTCTG AAGCCAGTTA CCTTCGAAA AAGAGTTGGT AGCTCTTGAT CCGCAAAACA TCCTCTCATA AACCATAGAC GCGAGAGGAC TTCGGTCAAT GGAAGCCTTT TTCTCAACCA TCGAGAAGCTA GCGCGTTTGT
8321	AACCAACCGT GGTAGCGGTG GTTTTTTGT TTGCAAGCAG CAGATTACGC GCACAAAAA AGGATCTCAA GAAGATCCCTT TTGGTGGGGA CCATGCCAC CAAAAAACA AACGTTCGTC GTCTAATGGG CGTCTTTTTT TCCTAGAGTT CTCTAGGAA
8401	TGATCTTTTC TAGGGGTCT GAGCTCAGT GGAACGAAA CTCACCTTAA GGGATTTTGG TCATGAGATT ATCAAAAAAG ACTAGAAAAG ATGCCCCAGA CTGGAGTCA CTTTGCCTTT GAGTGCATTT CCCTAAAAACC AGTACTCTAA TAGTTTTTCC
8481	ATCTTCACCT AGATCCCTTT AAATTAAAA TGAAGTTTAA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TAGAAGTGA TCTAGGAAAA TTTAATTTTT ACTTCAAAAA TTAGTTAGAT TTCAATATA CTCATTTGAA CCAGACTGTC
8561	TTACCAATGC TTAATCAGTG AGGCACTAT CTCAGCGATC TGCTATTTTC GTTCATCCAT AGTTGCCTGA CTCCCGCTCG AATGTTTACG AATTAGTCA CCGTGGATA GAGTCGCTAG ACAGATAAAG CAAGTAGGTA TCAAGGGACT GAGGGGCGAC
8641	TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGTGCA ATGATACCGC GAGACCCACG CTCACCGGCT ACATCTATTG ATGCTATGCC CTCCCGAATG GTACACGGG GTCAAGCAGT TACTATGGCG CTCTGGGTGC GAGTGGCGCA
8721	CCAGATTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGGAGAAG TGGTCCTGCA ACTTTATCCG CTTCCATCCA GGTCTAAATA GTCGTTATT GTCTGCTCGG CCTTCCGGCG TCGCTCTTC ACCAGGACGT TCAAAATAGGC GGAGGTAGT
8801	GTCTATTAT TCTTCCGGG AACCTAGAT AAGTAGTTCC CCAGTTAATA GTTTGGGCAA GGTGTGTGCC ATTGCTACAG CAGATAATTA ACAACGGCCC TTGATCTCA TTCAACAAG GGTCAATTAT CAAACCGCTT GCAACAAACG TAACGATGTC
8881	GCATCGTGGT GTACGGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGCGAGT TACATGATCC CGTAGCACCA CAGTGGGAGC AGCAAAACAT ACCGAAGTAA GTTCGAGGCA AGGTTTGCTA GTTCCGCTCA ATGTACTAGG

FIG. 3-Page 15

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7521	GGATTGTGT GAGTAGGTGT CATTTATTTC TGGGGGTGG GTTGGGGGAC GACAGCAAGG GGGAGGATTG GGAAGACAAT GCGTAACAGA CTCATCCACA GTAAGATAAG ACCCCCCACC CCACCCGCTC CTGCTGTCC CCTCTCTAAC CCTCTGTGTA
7601	ACGAGGCATG CTGGGGAGCT CTTCGCGTTC CTGCGTCACT GACTCGTGC GCTCGGTGCT TCGGCTGGGG CGAGCGGTAT TCGTCCGTAC GACCCCTCGA GAAGGGGAAG GAGCGAGTGA CTGAGGAGG CGAGCCAGCA AGCCGAGCGC GCTCGGCCATA
7681	CAGCTCACTC AAAGCGGTA ATACGGTTAT CCACAGATC AGGGATAAC GCAGGAAGA ACATGTGAGC AAAAGGCCAG GTCCAGTGAG TTTCGCCCAT TATGCCAATA GGTCCTTAG TCCCTATTG CGTCTTTCT TGTACACTCG TTTTCGGGTC
7761	CAAAAGGCCA GGAACGTA AAGGCGCG TTGCTGGCT TTTCCATAG GCTCCGCCG CCTGACGAGC ATCACAAAAA GTTTTCCGCT CCTTGGCATT TTTCCGGCGC AAGCACCGCA AAAAGGTATC CGAGGCGGGG GGACTGCTCG TAGTGTTTTT
7841	TCGACGCTCA AGTCAGAGGT GCGGAACCC GACAGACTA TAAAGATACC AGGCGTTTCC CCTTGGAAAG TCCCTCGTGC AGCTGGAGT TCAGTCTCCA CGCTTTGGG CTGTCTGTAT ATTCTATCG TCGGCAAGG GGGACCTTGG AGGGAGCAGG
7921	GCTCTCTGT TCGAGGCTG CGGCTTACCG GATACCTGTC CGCTTTCTC CCTTCCGGAA CGGTGGCGCT TTCTCAATGC CGAGAGGACA AGGCTGGGAC GCGGAATGCC CTATGCACG GCGGAAGAG GGAAGCCCTT CGCACCGCGA AAGAGTTACG
8001	TCAGGCTGTA GGTATCTCAG TTGCGTGTAG GTGTTGGCT CCAAGCTGGG CTGTGTGCAC GAACCCGCCG TTCAGCCGGA AGTGGGACAT CCATAGAGTC AAGCCACATC CAGCAAGCGA GGTTCGACCC GACACAGCTG CTTCGGGGGG AAGTGGGCT
8081	CCGCTGGCC TTATCCGTA ACTATCTCT TGAATCCAAC CCGGTACAGC AGCACTTATC GCCACTGGCA GGAGCCACTG GGCGAGCCG AATAGGCCAT TGAATAGCAG ACTGAGTTCG GGCATTTCTG TGTGAATAG CGGTGACCGT CGTGGGTGAC
8161	GTAACAGGAT TAGCAGCG AGGTATGTAG CGGTGTCTAC AGGTTCTTG AAGTGTGCG CTAACCTACCG CTACACTAGA CATTTGCTTA ATGCTCTCGC TCCATACATC CGCCAGGATC TCTCAAGAC TTACACACCG GATTGATGCC GATGTGATCT

FIG. 3-Page 14

pCMV-NS35

+2 N T T T S S E P A P S G C P P D S D A E S Y S S M P P
5361 ATACGACAAAC ATCTCTGAG CCCGCCCTT CTGGGTGCC CCCGACTCC GAGCTGAGT CCTATTCTC CATGCCCCC
TATGCTGTG TAGGAGACTC GGGGGGGGAA GACCGACGG GGGCTGAGG CTGCCACTCA GGATAAGGAG GTACGGGGGG

+2 L E G E P G D P D L S D G S W S T V S S E A N A E D V
BamHI

5441 CTGGAGGGG AGCTGGGA TCCGATCTT AGCGACGGT CATGTCAAC GGTCAGTAGT GAGGCCAAG CGGAGGATGT
GACCTCCCC TCGGACCCCT AGGCTAGAA TCGCTGCCCA GTACCAATTG CCAGTCATCA CTCGGGTTC GCCTCTACA

+2 V C C S M S Y S W T G A L V T P C A A E E Q K L P I
5521 CGTGTGCTGC TCAATGCTT ACTCTTGAC AGGCGCACTC GTCAAGCCGT GCGCGCGGA AGAACAGAAA CTGCCCATCA
GCACACGAGC AGTTACAGAA TGAGAACTG TCCGGCTGAG CAGTGGGGA CCGGGCGCT TCTTGTCTT GAGCGTAGT

+2 N A L S N S L L R H N L V Y S T T S R S A C Q R Q K
5601 ATGCACTAAG CAACGTGTG CTAGTCAAC ACAATTGCT GTATTCCAC ACCTCAGCA GTGCTTGCA AAGCAGAAC
TACGTGATTC GTTGACCAAC GATGCAGTGG TCTTAAACCA CATAAGTGG TGGAGTGGT CACGAACGCT TTCCGTCTTC

+2 K V T F D R L Q V L D S H Y Q D V L K E V K A A A S K
5681 AAAGTCACAT TTGACAGCT GCAAGTCTG GACAGCCAT ACCAGGACCT ACTCAAGGAG GTTAAAGCAG CGGCGTCAAA
TTTCAGTGTA AACTGTCTGA CGTTCAGAC CTGTGGTAA TGCTCTGCA TGAGTCTCTC CAATTCTCT CCGCGAGTTT

+2 V K A N L L S V E E A C S L T P P H S A K S K F G Y
5761 AGTGAAGCT AACTTGCTAT CCGTAGGGA ACCTTGAAG CTGACGCCCT CACACTCAG CAAATCCAA TTTGGTTATG
TCACCTCGGA TTGAAGGATA GGCATCTCT TCGAACGTCG GACTGCGGGG GTGTGACTCG GTTTAGGTTT AAACCAATAC

FIG. 3-Page 10

pCMV-NS35

+2	S	P	G	E	I	N	R	V	A	A	C	L	R	K	L	G	V	P	P	L	R	A	W	R	H	R	
6961	CTCTCCAGGT	GAAATCAATA	GGTGGCCGC	ATGCCTCAGA	AAACTTGGG	TACGGCCCTT	GCAGCTTGG	AGACACCGCG	GAGAGTGCA	CTTTAGTTAT	CCCACCGCG	TACGGAGTCT	TTTGAACCCG	ATGGCGGGA	CGCTCGAAC	TCTGTGCGCC											
+2	A	R	S	V	R	A	R	L	L	A	R	G	G	R	A	A	I	C	G	K	Y	L	F	N	W	A	V
7041	CCCGAGCGT	CCGGGTAGG	CTTCTGCCA	GAGGAGCAG	GGCTGCCATA	TGTGGCAAGT	ACCTCTTCAA	CTGGCGCAGTA	GGCCCTCGCA	GGCGCGATCC	GAAGACGGT	CTCTCCGTC	CCGACGGTAT	ACACCGTTCA	TGGAGAAAGTT	GACCCGTCATC											
+2	R	T	K	L	K	L	T	P	I	A	A	A	G	Q	L	D	L	S	G	W	F	T	A	G	Y	S	G
7121	AGAACAAAGC	TCAAATCAC	TCCAATAGC	CGCGGTGCC	AGCTGACTT	GTCGGGTGG	TTCACGGGTG	GCTACACGG	TCTTTGTTCC	AGTTTACGTG	AGTTTATCCG	CGCGACCGG	TGACCTGAA	CAGCGCGACC	AAGTCCCGAC	CGATGTGCGC											
+2	G	D	I	Y	H	S	V	S	H	A	R	P	R	W	I	W	F	C	L	L	L	A	A	G	V		
7201	GGGAGACATT	TATACACGG	TGCTCATGC	CGGCGCGCG	TGATCTGCT	TTTGCCTACT	CCTGTCTGCT	GCAGGGGTAG	CCCTCTGTAA	ATAGTGTGCG	ACAGAGTAGG	GGCCCGGGCG	ACCTAGACCA	AAACGGATCA	GGACGAAAGCA	CGTCCCGCATC											
+2	G	I	Y	L	L	P	N	R																			
7281	GCATCTACCT	CCTCCCCAAC	CGATGAAGT	TGGGTAAAC	ACTCGGGCT	AAAAAATAA	AAAAATCTAG	AAAGCGCGCG	GGTAGATGGA	GGAGGGGTG	GCTACTTCCA	ACCCCAATTG	TGAGGCGGGA	TTTTTTTTTT	TTTTTAGATC	TTTCCGCGCG											
	BAMHI MluI																										
7361	CAAGATATCA	AGGATCCACT	AGCGGTAGA	GCTCGGTGAT	CAGCCTCGAC	TGTGCCTTCT	AGTTGCCAGC	CATCTGTGTT	GTTCATAGT	TCTTAGGTGA	TGGCAATCT	CGAGGACTA	GTCCGAGGTG	ACACGGAAGA	TCAACGGTGG	GTAGACAAACA											
7441	TTGCCCTCG	CCCGTGCTT	CCTTGACCT	GGAAGTGCC	ACTGCCACTG	TCCTTTTCCTA	ATAAATGAG	GAAATTGCA	AACGGGGAG	GGGACGGAA	GGAAGTGGGA	CCTTCCACGG	TGAGGGTGAC	AGGAAAGGAT	TATTTTACTC	CTTTAAACGTA											

FIG. 3-Page 13

pCMV-NS35

+2	N	T	L	T	C	Y	I	K	A	R	A	A	C	R	A	A	G	L	Q	D	C	T	M	L	V	C	G
6401	AACACCTCA	CTTGCTACAT	CAAGCGCGG	GCAGCTGTC	GAGCCGAGG	GCTCCAGAC	TCACCATCG	TCGCTGTGG	TTGTGGAGT	GAACGATGA	GTTCGGGGC	CGTGGACAG	CTCGGGCTC	CGAGTCTCTG	ACGTGGTACG	AGCACACACC											
+2	D	D	L	V	V	I	C	E	S	A	G	V	Q	E	D	A	A	S	L	R	A	F	T	E	A	M	
6481	CGAGCACTA	GTGTTATCT	GTGAAGCGC	GGGGTCCAG	GAGCGCGG	CGAGCTGAG	AGCCTTCAG	GAGCTATCA	GCTGCTGAAT	CAGCAATAGA	CACCTTCGG	CCCCCAGTC	CTCCTCGCC	GCTCGGACTC	TGGGAAGTGC	CTCCGATACT											
+2	T	R	Y	S	A	P	G	D	P	P	Q	P	E	Y	D	L	E	L	I	T	S	C	S	S	N	V	
6561	CCAGGTACTC	CGCCCCCCT	GGGACCCCC	CACAAACAG	ATACCACTTG	GAGTCTATA	CATCATGTC	CTCACAACGTG	GGTCCATGAG	GGGGGGGGG	CCCTGGGGG	GTGTTGCTCT	TATGCTGAAC	CTCGAGTATT	GTAGTACGAG	GAGGTTGGAC											
+2	S	V	A	H	D	G	A	G	K	R	V	Y	Y	L	T	R	D	P	T	T	P	L	A	R	A	A	W
6641	TCAGTCCGCC	ACGACGGGCG	TGAAAGAGG	GTCTACTACC	TCACCGGTGA	CCCTACAACC	CCCCCTCGGA	GAGCTGCGTG	ACTCAGCGGG	TGCTCCCGCG	ACCTTTCTCC	CAGATGATGG	AGTGGCACT	GGGATGTTGG	GGGGAGCGCT	CTCGACGGCAC											
+2	E	T	A	R	H	T	P	V	N	S	W	L	G	N	I	I	M	F	A	P	T	L	W	A	R	M	
6721	GGAGACAGCA	AGACACACTC	CAGTCAATT	CTGGCTAGGC	AACATAATCA	TGTTTGGCC	CACACTGTGG	GGGAGATGA	CCTCTGTGCT	TCTGTGTGAG	GTCACTTAAG	GACCGATCCG	TTGTATTAGT	ACAAACGGGG	GTGTGACACC	CGCTCTCTACT											
+2	I	L	M	T	H	F	F	S	V	L	I	A	R	D	Q	L	E	Q	A	L	D	C	E	I	Y	G	A
6801	TACTGATGAC	CCATTCTTTT	AGGTCCTTA	TAGCGAGGA	CCAGCTTGAA	CAGGCGCTCG	ATTGCGAGAT	CTACGGGGCC	ATGACTACTG	GCTAAAGAAA	TCCAGGAAT	ATCGTCCCT	GGTCCAACTT	GTCCGGGAGC	TAACTCTCTA	GAATCCCGCG											
+2	C	Y	S	I	E	P	L	D	L	P	P	I	I	Q	R	L	H	G	L	S	A	F	S	L	H	S	Y
6881	TGCTATCTCA	TAGAACCACT	GGATCTACT	CCATCATTC	AAAGACTCCA	TGCGCTCAGC	GCATTTTCAC	TCACGGGCTA	ACGATGAGT	ATCTTGTGTA	CCTAGATGGA	GTTTCTAGT	ACCGGAGTGC	CGTAAAGTGC	AGGCTCTCAAT												

FIG. 3-Page 12

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+2	P S H I T A E A A G R R L I A R G S P P S V A S S S A
4801	TCCCTCCCAT ATAACAGCAG AGCGCGCG GCGAAGCTTG CCGAGGGGAT CACCCCTC TTGGCCGCTA AGGAGGGTA TATTGCTGTC TCGCCGGCC CGCTTCCAAC CGCTCCCTTA GTGGGGGAG ACACGGCTG AGGAGCGAT
+2	S Q L S A P S L K A T C T A N H D S P D A E L I E A N
4881	GCCAGCTATC CGCTCATCT CTCAAGCAA CTTGCACGGC TAACCATGAC TCCCTGATG CTGAGCTCAT AGAGGCCAAC CGGTGGATAG GCGAGTAGA GAGTTCGGT GAACTGGCG ATTGTACTG AGGGACTAC GACTCGAGTA TCTCCGTTG
+2	L L W R Q E M G G N I T R V E S E N K V V I L D S F D
4961	CTCCTATGGA GCGAGGAGG GCGCGCAAC ATCACCAGGG TTGAGTCAGA AAACAAAGTG GTGATTCTGG ACTCCTTCA GAGGATACCT CGCTCCTCTA CCGCGCGTTG TAGTGTCC CAACTCAGTCT TTTGTTTCAC CACTAAGACC TGAGGAAGCT
+2	P L V A E E D E R E I S V P A E I L R K S R R F A Q
5041	TCCGCTTGTG GCGGAGGAG GCGGAGGGA GATCTCCGA CCGGAGAAA TCCCTGCGAA GTCTCGGAGA TTCGCCCAGG AGGCGAACAC CGCCTCTCTC TGCTCGCCCT CTAGAGCAT GGGCGTCTTT AGGAGCCTT CAGAGCCTCT AAGCGGGTCC
+2	A L P V W A R P D Y N P P L V E T W K K P D Y E P P V
5121	CCCTGCGCTT TGGGCGGG CCGGACTATA ACCCCCGCT ACTGGAGACG TGAAGAAAG CCGACTACGA ACCACTGTG GGGACGGGCA AACCCGCGCC GGCTGATAT TGGGGGCGA TCACCTCTGC ACCTTTTTCG GGCTGATGCT TGGTGGACAC
+2	V H G C P L P P P K S P P V P P P R K K R T V V L T E
5201	GTCCATGGT GCGCGCTTCC ACCTCCAAAG TCCCTCTCTG TCCCTCCGCC TCGAAGAAG CCGACGGTGG TCCCTACCTGA CAGGTACCGA GCGGGGAAG TGGAGTTTC AGGGAGGAC ACGGAGGCG AGCCCTCTTC CCCTGCCACC AGGAGTACT
+2	S T L S T A L A E L A T R S F G S S S T S G I T G D
5281	ATAACCCCTA TCTACTGCT TGGCGGAGCT GCGCACCAGA AGCTTTGCA GTCTCTCAAC TTCCGGCATT ACGGCGACA TAGTTGGAT AGATGACGGA ACCGCTCGA CCGGTGGTCT TCGAAACCGT CCGAGGATTG AAGCCCGTAA TCCCGGCTGT

FIG. 3-Page 9

pcMV-NS35

+2	F	K	T	W	L	K	A	K	L	M	P	Q	L	P	G	I	P	F	V	S	C	Q	R	G	Y	K	G
4241	TTTAAGACCT	GGCTAAAGC	TAAGCTCATG	CCACAGCTGC	CTGGGATCCC	CTTTGTGTCC	TGCCAGCGCG	GGTATAAGGG	AAATTCTGGA	CCGATTTTGC	ATTGAGTAC	GGTGTGCGAG	GACCTTAGGG	GAACACAGG	ACGGTCGCGC	CCGATATCCC											
+2	V	W	R	G	D	G	I	M	H	T	R	C	H	C	G	A	E	I	T	G	H	V	K	N	G	T	
4321	GGTCTGGGGA	GGGAGCGGA	TCATGCACAC	TCGCTGCCAC	TGTGGAGCTG	AGATCACTGG	ACATGTCAA	AACGGACGGA	CCAGACCGCT	CCCTGCCCT	AGTACGTG	AGCGACGGT	ACACCTGCAC	TCTAGTGACC	TGTACAGTTT	TTGCGCTGCT											
+2	M	R	I	V	G	P	R	T	C	R	N	M	W	S	G	T	F	P	I	N	A	Y	T	T	G	P	C
4401	TCAGGATCGT	CGGTCTCTAGG	ACCTGCAGGA	ACATGTGGAG	TGGGACCTTC	CCCATTAATG	CCTACACCAC	GGGCCCTGT	ACTCCTAGCA	GCCAGGATCC	TGGAGCTCCT	TGTACACCTC	ACCTGGAAG	GGGTAAATTAC	GGATGTGGTG	CCGGGGGACA											
+2	T	P	L	P	A	P	N	Y	T	F	A	L	W	R	V	S	A	E	E	Y	V	E	I	R	Q	V	G
4481	ACCCCTCTTC	GTGGGCGGAA	CTACAGCTTC	CGGCTATGGA	GGGTGTCTGC	AGAGGAATAC	GTGGAGATAA	GGCAGGTGGG	TGGGGGGAAG	GACGGGGCTT	GATGTGCAAG	CGCGATACCT	CCACAGAGCG	TCTCCTTATG	CACCTCTAAT	CCGTCCACCC											
+2	D	F	H	Y	V	T	G	M	T	T	D	N	L	K	C	P	C	Q	V	P	S	P	E	F	F	T	
4561	GGACTTCAC	TACGTGAGG	GTATGACTAC	TGACAATCTT	AAATGCCCT	CGCAGGTCCC	ATCGCCCGAA	TTTTCACAG	CCTGAAGTG	ATGCATGCC	CATACTGATG	ACTGTTAGAA	TTTACGGGCA	CGGTCCAGGG	TAGCGGGCTT	AAAAAGTGT											
+2	E	L	D	G	V	R	L	H	R	F	A	P	P	C	K	P	L	L	R	E	E	V	S	F	R	V	G
4641	AAATGGACGG	GGTGGCGCTA	CATAGCTTTG	CGCCCGCTG	CAAGCCCTTG	CTCGGGGAGG	AGGTATCATT	CAGAGTAGGA	TTAACCTGCC	CCACCGGAT	GTAATCAAC	GCGGGGGGAC	GTTCCGGAAC	GACGCCCTCC	TCCATAGTAA	GTCTCATCT											
+2	L	H	E	Y	P	V	G	S	Q	L	P	C	E	P	E	P	D	V	A	V	L	T	S	M	L	T	D
4721	CTCCAGCAAT	ACCGGTAGG	GTGCGAATTA	CCTTGGGAGG	CCGAACCGGA	CGTGGCCGTG	TTGAGCTCCA	TGCTCACTGA	GAGTGTCTTA	TGGGCGATCC	CAGCGTTAAT	GGAACGCTCG	GGCTTGGCTT	GCACGGGCAC	AACTGCAGGT	AGCAGTGACT											

FIG. 3-Page 8

[illegible]

[illegible]

FIG. 3-Page 6

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+2	V	T	Q	T	V	D	F	S	L	D	P	T	F	T	I	E	T	I	T	L	P	Q	D	A	V	S	
2641	GTGACCCAG	ACATCGCAT	TCAGCCTTGA	CCCTAGCTTC	ACCATTCAGA	CAATCAGCT	CCCCAAGAT	GGTGTCTCCC	ACATGGGTG	TGTCAGTAA	AGTCGGAAC	GGGATGGAAG	TGGTAACCT	GTATGTGGA	GGGGTCTTA	CGACAGAGGG											
+2	R	T	Q	R	R	G	R	T	G	R	G	K	P	G	I	Y	R	F	V	A	P	G	E	R	P	S	G
2721	GCACTCAAG	TCGGGCGAG	ACTGGCAGG	GGAAGCCAG	CATCTACAGA	TTTGTGGCAG	CGGGCGAGG	CCCTTCGGG	CGTGAGTTG	AGCCCGCTCC	TCACCGTCCC	CCTTCGGTCC	GTAGATCTCT	AAACACCGTG	GCCCCCTCCG	GGGAGGCGGC											
+2	M	F	D	S	S	V	L	C	E	C	Y	D	A	G	C	A	W	Y	E	L	T	P	A	E	T	T	V
2801	ATGTTTCGACT	CGTCCCTCT	CTGTGACTGC	TATGACGCAG	GCTGTGCTTG	GTATCAGCTC	ACGCCGCGG	AGACTAGCT	TACAAGCTGA	CGAGGCAGA	GACACTCAG	ATACTGCGTC	CGACACGAAC	CATACTCGAG	TGGGGCGCGC	TCGTATGTCA											
+2	R	L	R	A	Y	M	N	T	P	G	L	P	V	C	Q	D	H	L	E	F	W	E	G	V	F	T	T
2881	TAGGCTACGA	GGCTACATGA	ACACCCCGGG	GTTCCCGTG	TGCCAGGACC	ATCTTGAATT	TTGGGAGGGC	GTCTTTACAG	ATCCGATGCT	CGCATGTACT	TGTGGGGCCC	CGAAGGGCAC	ACGGTCTCTG	TAGAACTTAA	AACCTCTCCG	CAGAAATGTG											
+2	G	L	T	H	I	D	A	H	F	L	S	Q	T	K	Q	S	G	E	N	L	P	Y	L	V	A	Y	Q
2961	GCCTCACTCA	TATAGATGCC	CACCTTTCTAT	CCCAGACAAA	GCAGAGTGCG	GAGAACCTTC	CTTACCTGGT	ACGGTACCAA	CGGAGTGAGT	ATATCTACGG	GTCAAGATA	GGGTCTCTTT	CGTCTCACCC	CTCTTGGAA	GAATGGACCA	TGGCATGGTT											
+2	A	T	V	C	A	R	A	Q	A	P	P	P	S	W	D	Q	M	W	K	C	L	I	R	L	K	P	T
3041	GCCACCGTGT	GGGTAGGGC	TCAAGCCCT	CCCCATCGT	GGGACCAAGT	GTGGAAGTGT	TTGATTGCGC	TCAAGCCCA	CGGTGGCACA	CGCGATCCCG	AGTTCGGGGA	GGGGTAGCA	CCCTGGTCTA	CACCTTCACA	AACTAAGCGG	AGTTCGGGTG											

FIG. 3-Page 5

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+2	A H G I D P N I R T G V R T I T T G S P I T Y S T Y G
2081	GTCATGGGA TCGATCCTAA CATCAGACCC GGGGTGAGAA CAATTACCAC TGGCAGCCCC ATCAGCTACT CCAGCTACGG CGAGTACCGT AGCTAGGATT GTAGTCCTGG CCGCACTCTT GTTAATGGT ACCGTCGGGG TAGTGCATGA GTGGGATGCC
+2	K F L A D G G C S G G A Y D I I I C D E C H S T D A
2161	CAAGTTCCTT CCGCAGGGGG GGTGCTCGG GGGCGCTTAT GACATAATA TTGTGAGGA GTGCCACTCC ACCGATGCCA GTTCAGGAA CCGCTGCCGC CCACGAGCCC CCGCGAATA CTGTATTATT AAACACTGCT CACGGTGAGG TGCGTACGGT
+2	T S I L G I G T V L D Q A E T A G A R L V V L A T A T
2241	CATCCATCTT GGCATTTGG ACTGCTCTTG ACCAAGCAGA GACTGGGGG GCGAGACTGG TTGTGCTGC CACGGCCACC GTAGTGAAA CCGGTAAACG TGACAGAAC TGGTTCTGCT CTGACGCCGC CGCTCTGACC AACACGAGCG GTGGCGGTGG
+2	P P G S V T V P H P N I F E V A L S T T G E I P F Y G
2321	CCTCCGGGCT CGCTCACTT GCCCATCC AACATCGAG AGTTGCTCT GTCCACCACC GGAGAGATCC CTTTTACGG GGAGGCCGA GGCAGTGACA CCGGTAGGG TTGTAGTCC TCCACGAGA CAGGTGGTG CCTCTCTAGG GAAAAATGCC
+2	K A I P L E V I K G G R H L I F C H S K K K C D E L
2401	CAAGGCTATC CGCCTCGAAG TAATCAAGG GGGGAGACAT CTCATCTTCT GTCAATCAAA GAAGAAGTGC GAGGAACTCG GTTCGGATAG GGGGAGCTTC ATTAGTTCC CCGCTCTGTA GAGTAGAAGA CAGTAAGTTT CTCTTTCAG CTGCTTGAGC
+2	A A K L V A L G I N A V A Y Y R G L D V S V I P T S G
2481	CCGAAAGCT GGTCCGATTTG CGATCAATG CCGTGGCTA CTACCGCGGT CTTCAGCTCT CCCTCATCCC GACGAGCGGC GGCGTTTCGA CCAGGGTAAC CCGTAGTTAC GGCACCGGAT GATGGCGGCA GAACCTGCACA GGCAGTAGGG CTGGTGCGCG
+2	D V V V V A T D A L M T G Y T G D F D S V I D C N T C
2561	GATCTTCTCG TCGTGGCAAC GGTAGCCCTC ATGACCGGCT ATACGGCGA CTTCGACTCG GTGATAGACT GCAATAGCTG CTACAACAGC AGCAGCGGTG GCTAAGGGAG TACTGGCGA TATGGCCGCT GAAGCTGACC CACTATCTGA CGTTAAGCAC

FIG. 3-Page 4

pCMV-NS35

1441	TATTTACAAA TTACATATA CAACAACGCC GTCCCCCGTG CCGCAGTTT TTATTAACA TAGCTGGGA TCTCGACAT ATAAATGTTT AAGTGAAT GTTGTGGG CAGGGGCAC GGGGCTCAA AATAATTTCT ATCGACCT AGAGCTGTA
1521	CTCGGGTAGG TGTTCGGAC ATGGGCTTT CTCCGTAGC GCGGACCTT CCACATCGA GCCCTGGTCC CATCCGTCCA GAGCCCATGC ACAAGGCGT TACCGGAA GAGGCCATG CCGCTCGAA GGTGTAGCT CCGGACCAGG GTAGGCAGT
1601	GCGGCTCATG CTGCTCGGC AGTCTTTGC TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCAAC CGCCAGTAC CAGCGAGCGG TCGAGGAAC AGGATTGCA CCTCGGTCT GAAATCCGTCT CGTGTACGG GTGTGGTGG
1681	AGTGTCCGC ACAAGGCCGT GCGGTAGGG TATGTCTGTG AAAATGAGT CCGAGATTGG GCTCGCACT GGAGGCAGAT TCACACGGCG TGTTCGGCA CCGCATCCC ATACACAGC TTTTACTGA GCCTCTAAC CGAGCGTGA CCTCCGCTTA
1761	GGAAGACTTA AGCAGCGGC AGAAGAAGT GCAGGCAGT GAGTCTTCT ATTCTGATA GAGTCAGAG TAACTCCCGT CCTTCTGAAT TCGTGGCG TCTTCTTA CCGTGGTGA CTCACAACA TAAGCTATT CTCAGTCTCC ATTGAGGGA
1841	TGCGTGCTG TTAACGGTGG AGGCAGTGT AGTCTGAGCA GTACTGGTGT CTGCGGGCG CGCCACCAGA CATAATAGCT ACGCCAGAC AATTGCCACC TCCCGTCACA TCAGACTGT CATGAGCAAC GAGCGGCG CGGTGGTCT GTATTATGA
+2	
1921	GACAGACTAA CAGACTGTTT CTTCATAGG GTCTTTTCTG CAGTCACGCT CGTCGACCTA AGAATTCACC ATGGGTGCA CTGTCTGATT GTCTGACAAG GAAAGTACC CAGAAAAGC GTCACTGGA GTCACTGGAT TCTTAAGTGT TACCGACGTA
+2	
2001	ATCGACTCA GGGCTAAG GTGCTAGTAC TCAACGCTTC TGTGTGCTGA ACATGGGT TTGGTCTTA CATGTCGAAG TAGTTCGAT CCCGATATC CAGCATCA GAGTGGGAG ACAACGAGT TGTGACCGA AACCAAGAT GTACAGTTC

M A A

EcoRI

FIG. 3-Page 3

pCMV-NS35

+2 G A K D V R C H A R K A V T H I N S V W K D L L E D N
5841 GGGGAAAGA GTCCGGTGG CATCCGAGAA AGGCGGTAA CACATCAAC TCGGTGTGA AGACCTTCT GGAAGCAAT
CCGGTTTCT CGAGGCAAG GTACGGTCTT TCCGGCATG GGTGTAGTTG AGGCACACT TTCTGGAGA CCTTCTGTTA

+2 V T P I D T T I M A K N E V F C V Q P E K G G R K P A
5921 GTAACACAA TAGACTATC CATCATGGCT AGAACGAGG TTTTGTGCT TCAGCTGAG AAGGGGGTC GTAAGCGAG
CAATTGGTT ATCTGTGATG GTATACCGA TTCTTGCTCC AAAAGACGA AGTGGACTC TTCCCCCCC CATTCGGTGG

+2 R L I V F P D L G V R V C E K M A L Y D V V T K L P
6001 TCGTCTATC GTTTCGCG ATCTGGCGT CCGGTGTCC GAAAGATGG CTTTGTACGA CTGTGTACA AAGTCCCT
AGCAGATAG CACAAGGGG TAGACCGCA CGGCAACG CTTTCTACC GAAACATGCT GCACCAATGT TTGAGGGGA

+2 L A V M G S S Y G F Q Y S P G Q R V E F L V Q A W K S
6081 TGGCGGTGAT GGGAAGCTCC TAGCGATTCC AATACTACC AGGACAGCG GTTGAATTCC TCGTCAAGC GTGGAAGTC
ACGGGACTA CCTTCGAGG ATCCTAAG TTATAGTG TCTGTGCC CAACCTAAG AGCAGTTGC CACCTTCAGG

+2 K K T P M G F S Y D T R C F D S T V T E S D I R T E E
6161 AAGAAACCC CAATGGGTT CTCTGATGAT ACCGGTGTG TTGACTCCAC AGTCACTGAG AGCGACATCC GTACGGAGA
TTCTTTTGG GTTACCCAA GAGCATACTA TGGCGACGA AACTGAGTG TCACTGACTC TCGCTGAGG CATGCTCT

+2 A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G
6241 GGAATCTAC CAATGTTGTG ACCTGACCC CCAAGGCCG GTGGCCATCA ACTCCCTCAC CGAGAGCTT TATGTTGGG
CCGTTAGATG GTTAAACAC TGGAGCTGG GTTTCGGGG CACGGTAGT TCAGGAGTTC TCGTGTAGG ATACAAACCC

+2 G P L T N S R G E N C G Y R R C R A S G V L T T S C G
6321 GCCTCTTAC CAATTCAAG GGGGAGAACT GCGGTATCG CAGGTGCCG GCGAGCGGG TACTGACAAC TAGTGTGGT
CGGAGATG GTTAAATTCC CCGCTCTTGA CGCGGATAG GTCCACGGG CCGTGGCGG ATGACTGTTG ATGACACCA

FIG. 3-Page 11

pCMV-NS35

721	GCCTGGCATT ATGCCAGTA CATGACCTTA CGGACTTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGTATTATAC CGGACCGTAA TACGGTTCAT GTACTTGAAT GCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG
801	CATGTGTATG CGGTTTGGC AGTACACCAA TGGGCGTGGA TAGGGTTTG ACTCACGGGG ATTTCCAAGT CTCACACCCA GTACCACTAC GCCAAACCG TCATGTGTT ACCCGCACT ATCCCAAC TCAGTCCGCC TAAAGTTCA GAGTGGGGT
881	TTGAGTCAA TGGGACTTTG TTTTGGCACC AAAATCAAGG GGACTTTCCA AAATCTCGTA ATAAACCCGC CCCGTTGACG AACTGCAGT ACCTCAAC AAAACCGTGG TTTTGGTTGC CCTGAAAGT TTTACAGCAT TATTGGGGCG GGGCAACTGC
961	CAAAATGGCG GTAGGCTGT ACGGTGGAG GTCTATATA GCAGACCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG GTTTACCGGC CATCCGCACA TCCACACCTC CAGATATATT CGTCTGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC
1041	CCATCCACG TGTTTGACC TCCATAGAAG ACACCGGAC CGATCCAGCG TCCGGGCGG GGAACGCTCC ATTGGAACCG GGTAGGTGCG ACAAACCTGG AGGTATCTTC TGTGGCCCTG GCTAGGTGCG AGGGCCGCGC CCTTGCACG TAACCTTGGC
1121	GGATTCCCG TGCCAAGAT GACCTAAGTA CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA CCTAAGGGCG ACGTCTCA CTGCATTAT GCGGGATATC TGAGATATCC GTGTGGGAA ACCGAGAATA CGTACGATAT
1201	CTGTTTGTG CTGGGGGCT ATACACCCGC GCTCCTTATG CTATAGTGA TGGTATAGCT TAGCCTATAG GTGTGGGTTA GACAAAAAC GAACCCGGA TATGTGGGG CGAGGAATAC GATATCCAT ACCATATCGA ATCGGATATC CACACCAAT
1281	TTGACCATTA TTCACCATC CCTATTGCT GAGCATACT TCCATTACTA ATCCATAACA TGGCTCTTTG GCACAACTAT AACTGGTAT AACTGGTAT GGGATAACCA CTGCTATGAA AGTAAATGAT TAGGTATTGT ACCGAGAAC GGTGTGATA
1361	CTCTATTGG TATATGCCAA TACTCTGCC TTCAGACAT GACACGGACT CTGTATTTT ACAGGATGG GTCCATTAT GAGATAACCG ATATAGGTT ATGACACAGG AAGTCTGTA CTGTGCTGTA GACATAAAA TCTCTACCC CAGTAAATA

FIG. 3-Page 2

pCMV-NS35

1	TCGGCGGTTT CGTGATGAC GGTGAAACC TCTGACACAT CAGCTCCCG GAGACGGTCA CAGCTTGCT GTAGCGGAT AGCGCGAAA GCCACTACTG CCACCTTTGG AGACTGTGTA CGTCGAGGC CTCTGCCAGT GTCGAACAGA CATTCGCCTA
81	CGCGGGAGCA GACAAAGCCG TCAGGCGGG TCAGCGGTG TTGGGGGTG TCGGGGCTGG CTTAACATATG CGGCATCAGA CGGCCCTCGT CTGTTTGGGC AGTCGGGCGC AGTCGCCAC AACGCCAC AGCCCCACC GAAITGATAC GCGGTAGTCT
161	GCACATTGTA CTGAGAGTGC ACCATATGAA GCCTTTTGC AAGCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCGG CGCTAACAT GACTCTCAG TGTATACTT CGAAAAACGT TTTCGGATCC GGAGGTTTT TCGGAGGAGT GATGAAGAC
241	AATAGCTCAG AGGCGAGGC GGCCTCGGC TCTGCATAA TAAAAAAT TACTCAGCA TGGGGCGGAG AATGGCGGA TTATCAGTC TCCGCTCCG CCGGAGCGG AGAGTATTT ATTTTTTTA ATCAGTCGCT ACCCGGCTC TTACCGGCT
321	ACTGGCGGG GAGGGAATTA TTGGCTATT GCCATTGCAT ACGTTGTATC TATATCATAA TATGTACAT TATATTGCT TGACCGGCGC CTCCTTTAAT AACCGATAAC CGGTACGTA TCCACATAG ATATAGTATT ATACATGTA ATATAACGA
401	CATCTCCAAT ATGACGCCA TGTGACATT GATTATTGAC TAGTTATTA TAGTAATCAA TTACGGGTC ATTAGTTCAT GTACAGTTA TACTGGCGGT ACAACTGTAA CTAATAACTG ATCAATAATT ATCATTAGT AATGCCCCAG TAATCAAGTA
481	AGCCCATATA TGGAGTTCG CGTTACATAA CTTACGGTAA ATGCGCGCC TGGGTGACC CCAAGGACC CCGGCCCAT TCGGGTAT ACCTCAAGC GCAATGTATT GAAIGCCATT TACGGGCGG ACCGACTGCC GGGTTGCTGG GGGGGGTAA
561	GACGTCAATA ATGAGGTATG TTCCCATAGT AACGCCAATA GGGACTTTC ATTGACGTCA ATCGGTGGAG TATTACGGT CTGCAGTTAT TACTGCATAC AAGGTATCA TTGGGTTAT CCCTGAAAGC TAACGTGAGT TACCCACUTC ATAAATGCCA
641	AAACTGCCA CTTGGCAGTA CATCACTGT ATCATAGCC AAGTCGCGC CCTATTGAC TCAATGACG TAAATGCC TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACG TTCAGGCGG GATAACTGC AGTTACTGCC ATTTACGGG

StuI

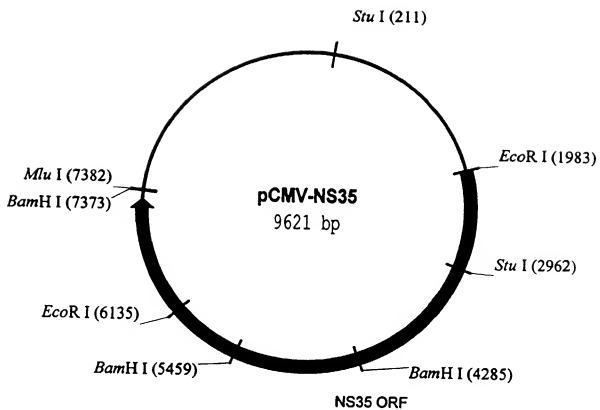


FIG. 2

Cloning Scheme for Generating pCMV-NS35

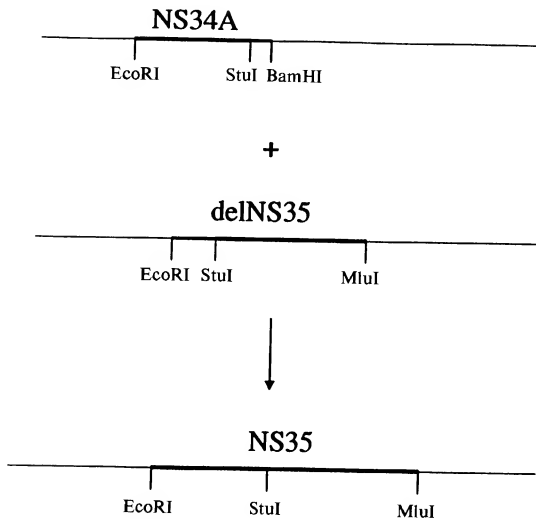


FIG. 1

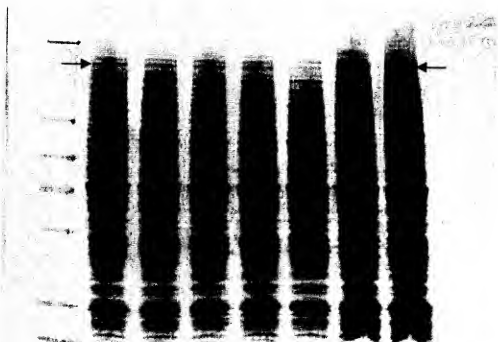


FIG. 23

5449 APAI,

5462 GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGACGTGAGCCT
CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
^ ^ ^ ^ ^

5467 BSSH2, 5478 XMNI, 5502 KHOI, 5511 AAT2,

5522 IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
ATCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
TAGGGGTTCCGAGCAGCGGGCTCCCGTCTGGACCCGAGTCGGGCCCATGGGAACCGGG
^ ^ ^ ^ ^

5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

5582 LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
GAGATACCGTTACTCCCCAGCCCCACCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

5642 ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAsp
CCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCGCGCAATTTGGGTAAAGGTCATCGAT
GGATCGACCCCGGGGTGTCTGGGGCCGCATCCAGCGGTTAAACCCATTCCAGTAGCTA
^ ^ ^ ^ ^

5650 APAI, 5696 CLAI,

5702 ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCCTCTT
TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCGCGGGGAGAA
^ ^ ^ ^ ^

5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,

5762 GlyGlyAlaAlaArgAlaOC AM
GGAGGCGCTGCCAGGGCCTAATAGTCGAC
CCTCCGCGACGGTCCCGGATTATCAGTG
^

5785 SALI,



A DCPHOENIX

APPL PARTS



371P
PCT Papers in a 371 Application
A...
Amendment Including Elections
ABST
Abstract
ADS
Application Data Sheet
AF/D
Affidavit or Exhibit Received
APPENDIX
Appendix

ARTIFACT
Artifact

BIB
Bib Data Sheet

CLM
Claim

COMPUTER
Computer Program Listing

CRFL
All CRF Papers for Backfile

DIST
Terminal Disclaimer Filed

DRW
Drawings

FOR
Foreign Reference

FRPR
Foreign Priority Papers

IDS
IDS Including 1449

NPL
Non-Patent Literature

OATH
Oath or Declaration

PET.
Petition

RETMAIL
Mail Returned by USPS

SEQLIST
Sequence Listing

SPEC
Specification

SPEC NO
Specification Not in English

TRNA
Transmittal New Application

CTNF
Count Non-Final

CTRS
Count Restriction

EXIN
Examiner Interview

M903
DO/EO Acceptance

M905
DO/EO Missing Requirement

NFDR
Formal Drawing Required

NOA
Notice of Allowance

PETDEC
Petition Decision

OUTGOING



1449
Signed 1449

892

ABN
Abandonment

APDEC
Board of Appeals Decision

APEA
Examiner Answer

CTAV
Count Advisory Action

CTEQ
Count Ex parte Quayle

CTFR
Count Final Rejection

INCOMING

AP.B
Appeal Brief

C.AD
Change of Address

N/AP
Notice of Appeal

PA...
Change in Power of Attorney

REM
Applicant Remarks in Amendment

XT/
Extension of Time filed separate

Internal

SRNT
Examiner Search Notes

CLMPTO
PTO Prepared Complete Claim Set

ECBOX
Evidence Copy Box Identification

WCLM
Claim Worksheet

WFEE
Fee Worksheet

File Wrapper

FWCLM
File Wrapper Claim

IIFW
File Wrapper Issue Information

SRFW
File Wrapper Search Info

Cloning Scheme for Generating pCMV-NS35

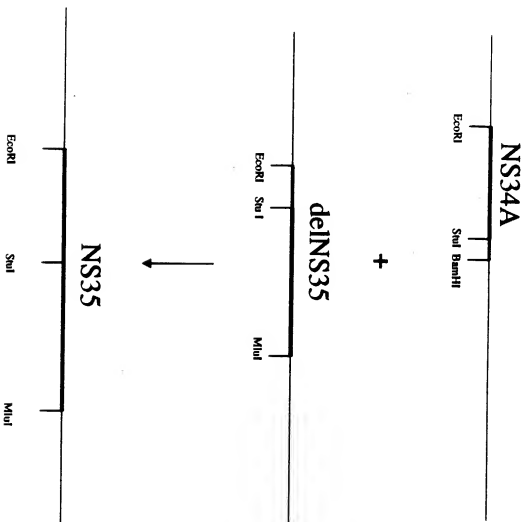


FIGURE 1